

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Novartis AG
- (B) STREET: Schwarzwaldallee 215
- (C) CITY: Basel
- (E) COUNTRY: Switzerland
- (F) POSTAL CODE (ZIP): 4058
- (G) TELEPHONE: +41 61 324 1111
- (H) TELEFAX: + 41 61 322 75 32

(ii) TITLE OF INVENTION: Rifamycin biosynthesis gene cluster

(iii) NUMBER OF SEQUENCES: 9

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5676 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

4043405
2043405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGTACCCGGT GTTCGCGACG GCGTTCGACG AGGCTTGC GA GCAGCTGGAC GTCTGTCTGG 60

CCGGCCGTGC CGGGCACCGC GTGCGGGACG TCGTGCTCGG CGAAGTGCCC GCCGAAACCG 120

GGCTGCTGAA CCAGACGGTC TTCACCCAAG CCGGGCTGTT CGCGGTGGAG AGCGCGCTGT 180

TCCGGCTCGC CGAATCCTGG GGTGTCCGGC CGGACGTGGT GCTCGGCCAC TCCATCGGGG 240

AGATCACCGC CGCGTATGCC GCGGGCGTCT TCTCGCTGCC GGACGCCGCC CGGATCGTCG 300

CGGCGCGCGG CCGGCTGATG CAGGCGCTGG CGCCGGGCGG GCGGATGGTC GCCGTCGCCG 360

CCTCCGAAGC CGAGGTGGCC GAACTGCTCG GCGACGGCGT GGAATCGCC GCCGTCAACG 420

GCCCTTCGGC GGTAGTCCTT TCCGGGGACG CGGACGCGGT CGTCGCGGCC GCCGCCCGCA 480

TGCGCGAGCG CGGGCACAAG ACCAAGCAGC TCAAGGTTTC GCACGCGTTC CACTCCGCGC 540

GGATGGCGCC GATGCTGGCG GAGTTCGCCG CCGAGCTGGC CGGCGTGACG TGGCGCGAGC 600

CGGAGATCCC GGTGGTCTCC AACGTGACCG GCCGGTTCGC CGAGCCCGGC GAACTGACCG 660

AGCCGGGCTA CTGGGCCGAG CACGTGCGGC GGCCGGTGCG GTTCGCCGAG GGCCTCGCGG 720

CCGCGACGGA GTCCGCGGCG TCGTGTTTCG TGGAGCTCGG GCCGGGGGCG GCGCTGACCG 780

CCCTCGTCGA GGAGACGGCC GAGGTCACCT GCGTCGCGGC CCTGCGGGAC GACCGCCCGG 840

AGGTCACCGC GCTGATCACC GCGGTGCGCG AGCTGTTTCGT CCGCGGGGTT GCGGTTCGATT 900

GGCCGGCCCT GCTGCCGCCG GTCACCGGGT TCGTCGACCT GCCGAAGTAC GCCTTCGACC 960

AGCAGCACTA TTGGCTGCAG CCCGCCGCGC AGGCCACGGA CGCGGCCTCG CTCGGGCAGG 1020

TCGCGGCCGA	CCACCCGCTG	CTGGGCGCGG	TGGTCCGGCT	GCCGCAGTCG	GACGGCCTGG	1080
TCTTCACCTC	GCGGCTGTCA	TTGAAATCGC	ACCCGTGGCT	GGCCGACCAC	GTCATCGGCG	1140
GGGTGGTGCT	CGTCGCGGGC	ACCGGGCTCG	TCGAGCTGGC	CGTCCGGGCC	GGGGACGAGG	1200
CCGGCTGCCC	GGTCCTCGAA	GAACCTCGTA	TCGAGGCTCC	GCTGGTCGTC	CCCACCACG	1260
GCGGGGTCCG	GATCCAGGTC	GTCGTGGGGG	CACCGGGGGA	GACCGGTTTCG	CGCGCGGTTCG	1320
AGGTGTACTC	CCTGCGCGAG	GACGCCGGTG	CCGAAGTGTG	GGCCCCGGCAC	GCCACCGGGT	1380
TCCTGGCTGC	GACGCCGTGC	CAGCACAAGC	CGTTCGACTT	CACCGCCTGG	CCGCCGCCCG	1440
GCGTCGAGCG	CGTCGACGTC	GAGGACTTCT	ACGACGGCTT	CGTCGACCGC	GGGTACGCCT	1500
ACGGGCCCGTC	GTTCCGGGGC	CTGCGGGCGG	TGTGGCGGCG	CGGCACGAA	GTGTTGCGCG	1560
AGGTGCCCCCT	GGCCGAGGAC	GACCGCGCGG	ACGCGGCCCG	GTTCCGGCATC	CACCCCGGCC	1620
TCCTGGACGC	CGCCCTGCAC	GCGGGCATGG	CCGGTGCCAC	CACCACGGAA	GAGCCCGGCC	1680
GGCCGGTGCT	GCCGTTGCCC	TGGAACGGCC	TGGTGCTGCA	CGCGGCCGGG	GCGTCCGCGC	1740
TGCGGGTCCG	GCTCGCCCCG	AGCGGTCCGG	ACGCCCTGTC	GGTCGAGGCC	GCGGACGAGG	1800
CCGGCGGTCT	CGTTGTGACG	GCGGACTCGC	TGGTCTCCCG	GCCGGTGTCG	GCCGAACAGC	1860
TGGGCGCGGC	GGCGAACCAC	GACGCGTTGT	TCCGCGTGGA	GTGGACCGAG	ATTTCCTCGG	1920
CTGGAGACGT	TCCGGCGGAC	CACGTCAAG	TGCTCAAGC	CGTCGGCGAG	GATCCCCCTGG	1980
AACTGACCGG	CCGGGTCTTG	GAGGCCGTGC	AGACCTGGCT	CGCCGACGCA	GCCGACGACG	2040
CTCGCCTGGT	CGTGGTGACC	CGCGGCGCCG	TCCACGAGGT	GACTGACCCG	GCCGGTGCCG	2100
CGGTGTGGGG	CCTGATCCGG	GCCGCGCAGG	CGGAAAACCC	GGACCGGATC	GTGCTGCTGG	2160

ACACCGACGG TGAAGTGCCG CTAGGCCGGG TGCTGGCCAC CGGCGAGCCC CAAACAGCCG 2220

TCCGAGGCGC CACGCTGTTC GCCCCGCGC TGGCCCGCGC CGAGGCCGCG GAGGCACCGG 2280

CAGTGACCGG CGGGACGGTC CTGATCTCGG GCGCCGGCTC GCTGGGCGCG CTCACCGCCC 2340

GGCACCTGGT CCCCCGGCAC GGAGTCCGGC GGCTGGTGCT CGTCAGCCGC CGTGGCCCCG 2400

ACGCCGACGG CATGGCCGAA CTGACCGCTG AACTCATCGC TCAGGGCGCC GAGGTCGCCG 2460

TAGTCGCTTG CGACCTGGCC GACCGGGACC AGGTCCGGGT ACTGCTGGCC GAGCACCGCC 2520

CGAACGCCGT CGTGACACG GCCGGTGTTC TCGACGACGG CGTCTTCGAG TCGCTGACGC 2580

GGGAGCGGCT GGCCAAGGTC TTCGCGCCCA AAGTTACTGC TGCCAATCAC CTCGACGAGC 2640

TGACCCGCGA ACTGGATCTT CGCGCGTTTC TCGTGTTCCTC CTCCGCCTCC GGGGTCTTCG 2700

GCTCCGCCGG GCAGGGCAAC TACGCCGCTG CCAACGCCTA CCTGGACGCC GTGGTCGCCA 2760

ACCGCCGGGC CGCGGGCCTG CCCGGCACAT CGCTGGCCTG GGGCCTGTGG GAACAGACCG 2820

ACGGGATGAC CGCGCACCTC GGCGACGCCG ACCAGGCGCG GGCGAGTCGC GCGGGGTCC 2880

TCGCCATCTC ACCCGCCGAA GGCATGGAGC TGTTGACGC AGCGCCGAC GGGCTCGTCG 2940

TCCCGGTCAA GCTGGACCTG CGCAAGACCC GCGCCGGCGG GACGGTGCCG CACCTGCTGC 3000

GCGGCCTGGT CCGCCCGGGA CGGCAGCAGG CCCGTCCGGC GTCCACTGTG GACAACGGAC 3060

TGGCCGGGCG ACTCGCCGGG CTCGCGCCGG CGGAGCAGGA GGCGCTGCTG CTCGACGTGC 3120

TCCGCACGCA GGTGCGCTG GTGCTCGGGC ACGCCGGGCC GGAGGCCGTC CGCGCGGACA 3180

CGGCGTTCAA GGACACCGGC TTCGACTCGC TGACGTCGGT GGAAGTGC GC AACC GGCTGC 3240

GCGAGGCGAG CGGGCTGAAG CTGCCC GCGA CGCTCGTCTT CGACTACCCG ACGCCGGTGC 3300

CGCTGGCCCC CTACCTGCGT GACGAATTG GCGACACGGT GGCAACAACCT CCGGTGGCCA 3360

CCGCGGCCGC AGCGGACGCC GCGAGCCGA TCGCCATCGT CGGCATGGCG TGCCGGCTGC 3420

CGGGCGGGGT CACCGATCCC GAAGGCCTGT GCGCCTGGT GCGCGACGGC CTCGAAGGGC 3480

TGTCTCCCTT CCCCAGGAC CGGGGCTGGG ACCTGGAGAA CCTGTTGAC GACGACCCCG 3540

ACCGCTCCGG CACGACGTAC ACCAGCCGGG GCGGGTTCCT CGACGGCGCC GGCCTGTTGC 3600

ACGCGGGCTT CTTCGGGATT TCGCCGCGCG AGGCGCTGGC CATGGACCCG CAGCAGCGGC 3660

TGCTGCTCGA GCGGCCTGG GAAGCCCTCG AAGGCACCGG TGTCGACCCG GGCTCGTTGA 3720

AGGCGCCGA CGTCGGGGTG TTCGCCGGG TGTCCAACCA GGGCTATGGG ATGGGCGCGG 3780

ATCCGGCCGA ACTGGCGGGG TACGCGAGCA CGGCGGGCGC TTCGAGCGTC GTCTCGGGCC 3840

GAGTCTCGTA CGTCTTCGGG TTCGAAGGAC CGGCGGTAC GATCGACACG GCTTGCTCGT 3900

CGTCGCTGGT GCGGATGCAC CTGGCCGGG AGGCGCTGCG GCAGGGCGAG TGCTCGATGG 3960

CCCTGGCCCG TGGCGTCACG GTGATGGGA CGCCCGCAC GTTCGTGGAG TTCGGAAGC 4020

AGCGCGGCCT GCGCGCGAC GGCCGGTGCA AGGCCTACGC CGAAGGCGCG GACGGCACGG 4080

GCTGGGCCGA GGGCGTCGGG GTCGTGTCG TGGAGCGGCT GTCGGTGGCG CGCGAGCGCG 4140

GGCACC GG GTCTEGCGTG CTGCGCGCA GCGCGGTCAA CTCCGACGGC GCGTCCAACG 4200

GCCTGACCGC CCCCACGGG CCGTCGAGC AACGGGTGAT CCGCCGGGCC CTGGCCGGCG 4260

CCGGCCTCGA ACCGTCCGAT GTGGACATCG TGGAAGGGCA CGGCACCGG ACGGCGCTGG 4320

GCGACCCGAT CGAGGCGCAG GCCCTGCTGG CCACCTACGG CAAGGACCGC GACCCGAGA 4380

CGCCGTTGTG GCTGGGGTCG GTGAAGTCGA ACTTCGGCCA CACGCAGTCC GCGGCCGGCG 4440

TGGCCGGGGT GATCAAGATG GTGCAGGCGC TGCGCCACGG CGTCATGCCG CCCACCCTGC 4500

ACGTGGACCG GCCCACCAGC CAGGTCGACT GGTCCGCGGG GGCCGTCGAA GTGCTGACCG 4560

AGGCACGGGA GTGGCCGCGG AACGGCCGTC CGCGCCGGGC CGGGGTGTCC TCGTTCGGGA 4620

TCAGCGGCAC GAACGCCCAC CTGATCATCG AAGAAGCACC GGCCGAGCCA CAGCTTGCCG 4680

GACCACCGCC GGACGGCGGT GTGGTGCCGC TGGTCGTCTC GGCTCGCAGC CCCGGTGCCC 4740

TGGCCGGTCA GGCGCGTCGG CTGGCCACGT TCCTCGGCGA CGGGCCCCCTT TCCGACGTG 4800

CCGGTGCGCT GACGAGCCGC GCCCTGTTCG GCGAGCGCGC GGTCGTCTGT GCGGATTCGG 4860

CCGAGGAAGC CCGCGCCGGT CTGGGCGCAC TGGCCCGCGG CGAAGACCGC CCGGGCCTGG 4920

TCCGCGGCCG GGTGCCCCGCG TCCGGCCTGC CGGGCAAGCT CGTGTGGGTG TTCCCCGGGC 4980

AGGGGACGCA GTGGGTGGGC ATGGGCCGCG AACTCCTCGA AGAGTCTCCG GTGTTGCGCG 5040

AGCGGATCGC CGAGTGTGCG GCCGCGCTGG AGCCGTGGAT CGGCTGGTCG CTGTTGACG 5100

TCCTCCGTGG CGACGGTGAC CTCGATCGGG TCGATGTGCT GCAGCCCGCG TGCTTTGCGG 5160

TGATGGTCGG CTGGCCCGCG GTGTGGTCCT CGGCCGGGGT GGTCCCCGAT GCGGTGCTCG 5220

GCCACTCCCA GGGTGAGATC GCCCGGGCGT GCGTGTCTGG TCGTTGTCTG CTGGAGGATG 5280

CGGCGAAGGT GGTGCCCCTG CGCAGCCAGG CCATCGCCGC GAAGCTCTCC GGCCGCGGCG 5340

GGATGGCTTC GGTGCGCTTG GGCGAAGCCG ATGTGGTGTG GCGGCTGGCG GACGGGGTCG 5400

AGGTGGCTGC CGTCAACGGT CCGGCGTCCG TGGTGATCGC GGGGGATGCC CAGGCCCTCG 5460

ACGAAACGCT GGAAGCGCTG TCCGGTGCGG GAATCCGGGC TCGGCGGGTG GCGGTGGACT 5520
ACGCCTCGCA CACCCGGCAC GTCGAAGACA TCGAAGACAC CCTCGCCGAA GCGCTGGCCG 5580
GGATCGACGC CCGGGCGCCG CTGGTGCCGT TCCTCTCCAC CCTCACCGGC GAGTGGATCC 5640
GGGACGAGGG CGTCGTGGAC GGCGGCTACT GGTACC 5676

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1891 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Tyr Pro Val Phe Ala Thr Ala Phe Asp Glu Ala Cys Glu Gln Leu Asp
1 5 10 15

Val Cys Leu Ala Gly Arg Ala Gly His Arg Val Arg Asp Val Val Leu
20 25 30

Gly Glu Val Pro Ala Glu Thr Gly Leu Leu Asn Gln Thr Val Phe Thr
35 40 45

Gln Ala Gly Leu Phe Ala Val Glu Ser Ala Leu Phe Arg Leu Ala Glu
50 55 60

Ser Trp Gly Val Arg Pro Asp Val Val Leu Gly His Ser Ile Gly Glu
65 70 75 80

Ile Thr Ala Ala Tyr Ala Ala Gly Val Phe Ser Leu Pro Asp Ala Ala
85 90 95

Arg Ile Val Ala Ala Arg Gly Arg Leu Met Gln Ala Leu Ala Pro Gly
100 105 110

Gly Ala Met Val Ala Val Ala Ala Ser Glu Ala Glu Val Ala Glu Leu
115 120 125

Leu Gly Asp Gly Val Glu Leu Ala Ala Val Asn Gly Pro Ser Ala Val
130 135 140

Val Leu Ser Gly Asp Ala Asp Ala Val Val Ala Ala Ala Arg Met
145 150 155 160

Arg Glu Arg Gly His Lys Thr Lys Gln Leu Lys Val Ser His Ala Phe
165 170 175

His Ser Ala Arg Met Ala Pro Met Leu Ala Glu Phe Ala Ala Glu Leu
180 185 190

Ala Gly Val Thr Trp Arg Glu Pro Glu Ile Pro Val Val Ser Asn Val
195 200 205

Thr Gly Arg Phe Ala Glu Pro Gly Glu Leu Thr Glu Pro Gly Tyr Trp
210 215 220

Ala Glu His Val Arg Arg Pro Val Arg Phe Ala Glu Gly Val Ala Ala
225 230 235 240

Ala Thr Glu Ser Gly Gly Ser Leu Phe Val Glu Leu Gly Pro Gly Ala
245 250 255

Ala Leu Thr Ala Leu Val Glu Glu Thr Ala Glu Val Thr Cys Val Ala
260 265 270

2060103"593400"

Ala Leu Arg Asp Asp Arg Pro Glu Val Thr Ala Leu Ile Thr Ala Val
275 280 285

Ala Glu Leu Phe Val Arg Gly Val Ala Val Asp Trp Pro Ala Leu Leu
290 295 300

Pro Pro Val Thr Gly Phe Val Asp Leu Pro Lys Tyr Ala Phe Asp Gln
305 310 315 320

Gln His Tyr Trp Leu Gln Pro Ala Ala Gln Ala Thr Asp Ala Ala Ser
325 330 335

Leu Gly Gln Val Ala Ala Asp His Pro Leu Leu Gly Ala Val Val Arg
340 345 350

Leu Pro Gln Ser Asp Gly Leu Val Phe Thr Ser Arg Leu Ser Leu Lys
355 360 365

Ser His Pro Trp Leu Ala Asp His Val Ile Gly Gly Val Val Leu Val
370 375 380

Ala Gly Thr Gly Leu Val Glu Leu Ala Val Arg Ala Gly Asp Glu Ala
385 390 395 400

Gly Cys Pro Val Leu Glu Glu Leu Val Ile Glu Ala Pro Leu Val Val
405 410 415

Pro Asp His Gly Gly Val Arg Ile Gln Val Val Val Gly Ala Pro Gly
420 425 430

Glu Thr Gly Ser Arg Ala Val Glu Val Tyr Ser Leu Arg Glu Asp Ala
435 440 445

Gly Ala Glu Val Trp Ala Arg His Ala Thr Gly Phe Leu Ala Ala Thr
450 455 460

Pro Ser Gln His Lys Pro Phe Asp Phe Thr Ala Trp Pro Pro Pro Gly

465	470	475	480
Val Glu Arg Val Asp Val Glu Asp Phe Tyr Asp Gly Phe Val Asp Arg			
485	490	495	
Gly Tyr Ala Tyr Gly Pro Ser Phe Arg Gly Leu Arg Ala Val Trp Arg			
500	505	510	
Arg Gly Asp Glu Val Phe Ala Glu Val Ala Leu Ala Glu Asp Asp Arg			
515	520	525	
Ala Asp Ala Ala Arg Phe Gly Ile His Pro Gly Leu Leu Asp Ala Ala			
530	535	540	
Leu His Ala Gly Met Ala Gly Ala Thr Thr Thr Glu Glu Pro Gly Arg			
545	550	555	560
Pro Val Leu Pro Phe Ala Trp Asn Gly Leu Val Leu His Ala Ala Gly			
565	570	575	
Ala Ser Ala Leu Arg Val Arg Leu Ala Pro Ser Gly Pro Asp Ala Leu			
580	585	590	
Ser Val Glu Ala Ala Asp Glu Ala Gly Gly Leu Val Val Thr Ala Asp			
595	600	605	
Ser Leu Val Ser Arg Pro Val Ser Ala Glu Gln Leu Gly Ala Ala Ala			
610	615	620	
Asn His Asp Ala Leu Phe Arg Val Glu Trp Thr Glu Ile Ser Ser Ala			
625	630	635	640
Gly Asp Val Pro Ala Asp His Val Glu Val Leu Glu Ala Val Gly Glu			
645	650	655	
Asp Pro Leu Glu Leu Thr Gly Arg Val Leu Glu Ala Val Gln Thr Trp			
660	665	670	

6060708090100110120130140150160170180190200210220230240250260270280290300310320330340350360370380390400410420430440450460470480490500510520530540550560570580590600610620630640650660670

Val Leu Asp Asp Gly Val Phe Glu Ser Leu Thr Arg Glu Arg Leu Ala
850 855 860

Lys Val Phe Ala Pro Lys Val Thr Ala Ala Asn His Leu Asp Glu Leu
865 870 875 880

Thr Arg Glu Leu Asp Leu Arg Ala Phe Val Val Phe Ser Ser Ala Ser
885 890 895

Gly Val Phe Gly Ser Ala Gly Gln Gly Asn Tyr Ala Ala Ala Asn Ala
900 905 910

Tyr Leu Asp Ala Val Val Ala Asn Arg Arg Ala Ala Gly Leu Pro Gly
915 920 925

Thr Ser Leu Ala Trp Gly Leu Trp Glu Gln Thr Asp Gly Met Thr Ala
930 935 940

His Leu Gly Asp Ala Asp Gln Ala Arg Ala Ser Arg Gly Gly Val Leu
945 950 955 960

Ala Ile Ser Pro Ala Glu Gly Met Glu Leu Phe Asp Ala Ala Pro Asp
965 970 975

Gly Leu Val Val Pro Val Lys Leu Asp Leu Arg Lys Thr Arg Ala Gly
980 985 990

Gly Thr Val Pro His Leu Leu Arg Gly Leu Val Arg Pro Gly Arg Gln
995 1000 1005

Gln Ala Arg Pro Ala Ser Thr Val Asp Asn Gly Leu Ala Gly Arg Leu
1010 1015 1020

Ala Gly Leu Ala Pro Ala Glu Gln Glu Ala Leu Leu Leu Asp Val Val
1025 1030 1035 1040

Arg Thr Gln Val Ala Leu Val Leu Gly His Ala Gly Pro Glu Ala Val
1045 1050 1055

Arg Ala Asp Thr Ala Phe Lys Asp Thr Gly Phe Asp Ser Leu Thr Ser

1060	1065	1070
Val Glu Leu Arg Asn Arg Leu Arg Glu Ala Ser Gly Leu Lys Leu Pro		
1075	1080	1085
Ala Thr Leu Val Phe Asp Tyr Pro Thr Pro Val Ala Leu Ala Arg Tyr		
1090	1095	1100
Leu Arg Asp Glu Phe Gly Asp Thr Val Ala Thr Thr Pro Val Ala Thr		
1105	1110	1115 1120
Ala Ala Ala Ala Asp Ala Gly Glu Pro Ile Ala Ile Val Gly Met Ala		
1125	1130	1135
Cys Arg Leu Pro Gly Gly Val Thr Asp Pro Glu Gly Leu Trp Arg Leu		
1140	1145	1150
Val Arg Asp Gly Leu Glu Gly Leu Ser Pro Phe Pro Glu Asp Arg Gly		
1155	1160	1165
Trp Asp Leu Glu Asn Leu Phe Asp Asp Asp Pro Asp Arg Ser Gly Thr		
1170	1175	1180
Thr Tyr Thr Ser Arg Gly Gly Phe Leu Asp Gly Ala Gly Leu Phe Asp		
1185	1190	1195 1200
Ala Gly Phe Phe Gly Ile Ser Pro Arg Glu Ala Leu Ala Met Asp Pro		
1205	1210	1215
Gln Gln Arg Leu Leu Leu Glu Ala Ala Trp Glu Ala Leu Glu Gly Thr		
1220	1225	1230
Gly Val Asp Pro Gly Ser Leu Lys Gly Ala Asp Val Gly Val Phe Ala		
1235	1240	1245
Gly Val Ser Asn Gln Gly Tyr Gly Met Gly Ala Asp Pro Ala Glu Leu		
1250	1255	1260

Asp Pro Ile Glu Ala Gln Ala Leu Leu Ala Thr Tyr Gly Lys Asp Arg
1445 1450 1455

Leu Pro Gly Lys Leu Val Trp Val Phe Pro Gly Gln Gly Thr Gln Trp

1650	1655	1660	
Val Gly Met Gly Arg Glu Leu Leu Glu Glu Ser Pro Val Phe Ala Glu			
1665	1670	1675	1680
Arg Ile Ala Glu Cys Ala Ala Ala Leu Glu Pro Trp Ile Gly Trp Ser			
	1685	1690	1695
Leu Phe Asp Val Leu Arg Gly Asp Gly Asp Leu Asp Arg Val Asp Val			
	1700	1705	1710
Leu Gln Pro Ala Cys Phe Ala Val Met Val Gly Leu Ala Ala Val Trp			
	1715	1720	1725
Ser Ser Ala Gly Val Val Pro Asp Ala Val Leu Gly His Ser Gln Gly			
	1730	1735	1740
Glu Ile Ala Ala Ala Cys Val Ser Gly Ala Leu Ser Leu Glu Asp Ala			
1745	1750	1755	1760
Ala Lys Val Val Ala Leu Arg Ser Gln Ala Ile Ala Ala Lys Leu Ser			
	1765	1770	1775
Gly Arg Gly Gly Met Ala Ser Val Ala Leu Gly Glu Ala Asp Val Val			
	1780	1785	1790
Ser Arg Leu Ala Asp Gly Val Glu Val Ala Ala Val Asn Gly Pro Ala			
	1795	1800	1805
Ser Val Val Ile Ala Gly Asp Ala Gln Ala Leu Asp Glu Thr Leu Glu			
	1810	1815	1820
Ala Leu Ser Gly Ala Gly Ile Arg Ala Arg Arg Val Ala Val Asp Tyr			
1825	1830	1835	1840
Ala Ser His Thr Arg His Val Glu Asp Ile Glu Asp Thr Leu Ala Glu			
	1845	1850	1855

Ala Leu Ala Gly Ile Asp Ala Arg Ala Pro Leu Val Pro Phe Leu Ser
1860 1865 1870

Thr Leu Thr Gly Glu Trp Ile Arg Asp Glu Gly Val Val Asp Gly Gly
1875 1880 1885

Tyr Trp Tyr
1890

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GAATTCAGG CCGTCGACGG CTGCGACATC GCGGTCTTCC GGTGGTCGCA CCGCACGAAG 60
ATCGCCGAAT AAGAATTTCC GGATCTCCCA CGGGAAAGGT TTCCATGACC GACGCAATAT 120
CCTTCGAGGT GCCGTGGGAC CGGACCGACA AGTTCGACCC GCCCGCGGTG TTCGACTCTC 180
TGCGCGAAGA ACGTCCGCTC GCGAAGATGG TTTACCCGGA TGGGCACGTC GGCTGGATCG 240
TTTCCAGCTA CGAGCTGGTC CGCGAGGTCC TCAGCGACCT GCGGTTTCAGC CACAGCTGCG 300
AAGTCGGCCA CTTCCCGGTG ACCCACCAGG GCCAGGTCAT CCCGACCCAC CCGCTGATCC 360

CCGGCATGTT CATCCACATG GACCCGCCCC AGCACACGCG CTACCGCAAG CTGCTGACCG 420

GCGAGTTCAC CGTCCGCCGC GCCAGCAGGC TGATCCCGCG GGCCGAGGCC GTGGCCGCCG 480

AGCAGATCGA GGTCATGCGG GCCAAGGGCG CCCCCGCGGA CGTGGTCATG GACTTCGCCA 540

AGCCGCTGGT GCTGCGGATG CTGGGCGAGC TCGTCGGCCT GCCCTACGAG GAACGCGACC 600

GGTACGTGCC CGCGGTGACC CTCCTGCACG ACGCCGAAGC GGACCCGGCC GAGGCCGCGG 660

CCGCCTACGA GGTGGCCGGG AAGTTCTTCG ACGAGGTCAT CGAGCGCCGC CGGCAGCGGC 720

CCCAGGACGA CCTCATCAGC TCGCTCGTCA CCGAGGACCT GACCCAGGAG GAGCTGCGCA 780

ACATCGTCAC CCTGCTGCTG TTCGCCGGGT ACGAGACCAC CGAGGGCGCG CTCGCCACCG 840

GCGTCTTCGC GCTGCTGCAC CACACCGATC AGCTGGCGGC ACTGCGCGCG GAGCCGGAAG 900

AGCTCGACGC CGCGATCGAA GAGCTGCTGC GCTACCTGAC CGTCAACCAG TACCACACCT 960

ACCGCACCGC GCTGGAGGAC GTGAAGCTGG AGGGCGAGCT GATCAAGAAG GGCGACACGG 1020

TGACGGTGTC GCTGCCCCGC GCCAACCGCG ACCCGGCCAA GTTCGGCTGT CCCGCGGAGC 1080

TCGACATCGA GCGGGACACC TCCGGCCACG TCGCGTTCGG CTTCGGCATC CACCAGTGCC 1140

TGGGCCAGAA CCTGGCGCGC ATCGAGCTGC GGGCCGGCTT CACGGCGCTC CTGCGGGCGT 1200

TCCCCGAGCT CCGGCTGGCC GTCCCGGCCG ACGAGGTTCC GCTGCGGCTG AAGGGTTCCG 1260

TCTTCTCGGT GAAGAAGCTG CCCGTCTCCT GGTGAGCGTT CTCCCCCTCG AACACCCGAA 1320

AGGATCTGCG GCACAGTGCG CACCGATCTC ATCAAGCCAC TTCACGTCGC ACTCCTGGAG 1380

AACGCGACCC GCTTCGCCCG CAAGCCGGCC TTCGCCGACG ACCACCGGAC GGTCACCTAC 1440

GGCGACCTCG AGGCGCGGAC GCGCCGGCTG GCCGGGCACC TGGCCGGCCT CGGTGTCCGG 1500

40445504050

CACGGCGACC GGGTGGCGAT CTGCCTCGGC AACCGGGTGT CCACTGTGGA GAGTTACTTC 1560

GCGATCCTGC GCGCGGGTGC CGTCGGCGTG CCGCTCAACC CCGGTTTCGGC GACGGCCGAG 1620

CTCGAGCACC CGCTGACCGA CAGCGGCGCC ACGGTGGTCG TCACCGACGC CGCCCAGGCG 1680

GCCCCGGCTCC GGCTCGCGCC GCACGTCGAG CTGCTGGTGA CCGGCGACGA CGTCCCGGAG 1740

GGCGCCCACT CCTACGACGA ACTCGCCCTC AGCGAACCGG CCGAGCCCCG CGCGGACGAC 1800

CTCGAGCTCG ACGAGCCGGC GTGGATGTTT TACACGTCGG GCACGACCGG GCGGCCCCAAG 1860

GGCGTCGTGT CCACGCAGCG CAACTGCCTC TGGTCCGTG CTTCCTGCTA CGTGCCGTTC 1920

CCCCGGTTGT CGGACCAGGA CCGGGTGCTC TGGCCGCTCC CGCTGTTCCA CAGCCTTTTCG 1980

CACATCGCCT GCGTCTGTC CGCCACCGTG GTCGGGGCCA GCGTCCGGAT CGCCGACGGC 2040

AGCTCCGCCG ACGACGTGAT GCGGCTGATC GAGGCGGAGA GCTCGACCTT CCTGGCCGGC 2100

GTGCCGACCA CCTACCACCA CCTGGTGCGG GCCGCCCGGC AGCGCGGTTT CTCCGCGCCG 2160

AGCCTGCGGA TCGGCCTGGC CGGGGGCGCG GTCCTCGGCG CCGGGCTGCG AAGCGAGTTC 2220

GAAGAGACCT TCGGGGTCCC GCTGATCGAC GCCTACGGCA GCACCGAGAC CTGCGGGGCG 2280

ATCACCATGA ACCCGCCGGA CGGCGCCCGC GTCGAGGGCT CGTGCGGCTT GGCCGTGCCG 2340

GGCGTCGACG TCGGGTTCGT CGACCCCGAC ACCGGGCTCG ACGTCCCCGC CGGCGAGGAG 2400

GGCGAGGTCT GGGTCAGCGG GCCGAACGTC ATGCTCGGCT ACCACAACAG CCCGAGGCG 2460

ACCGCCGCGG CGATGCGGGA CGGCTGGTTC CGGACCGGGG ACCTGGCCCG CCGCGACGAC 2520

GCCGGTTACT TCACCATCTG CGGCCGGATC AAGGAACTCA TCATCCGCGG CGGCGCGAAC 2580

20250323 15:34:00

ATCCACCCCG GCGAGGTCTGA GCGCGTCTTG CGCACGGTCG ACGGCGTCGC GGACGCGGCG	2640
GTCGGCGGTG TGCCGCACGA CACGCTCGGC GAGGTGCCCG TCGCTACGT CATCCCCGGA	2700
CCGACCGGTT TCGATCCTGC GCGGTTGATC GAGAAGTGCC GCGAACAGCT GTCCGCCTAC	2760
AAGGTGCCCG ACCGGATCCT CGAGGTGCGC CACATTCCCC GGACCGCGTC GGGCAAGATC	2820
CGGCGCGGGC TGCTGACCGA CGAGCCCGCG CAGCTGCGGT ACGCCGCGAC CGAACACGAG	2880
GAACAGTCCC GGCACGCCGA CGAGTCCGTC GCGGCGGCGC TCGCGCGCGC ACTGTCCGGT	2940
TTGGACGAAC GCGCCAGTG CGAGCTCCTG GAAGACCTCG TCCGCACCCA GGCGGCCGAC	3000
GTGCTGGGGC AGCCGGTCCC GGACGGGCGT GCGTTCCGCG ACCTCGGCTT CACGTCGCTG	3060
GCCATCGTGG AGCTGCGCAA CCGGCTGACC GAGCACACCG GGCTCTGGCT GCCCGCCAGC	3120
GCCGTCTTCG ACCACCCAC GCCGGCGGCG CTGGCCGCC GCGTCCGGC TGAGCTCCTC	3180
GGGATCACGC AGGCCGTCGC GGAGCCGGTC GTCGCGGCCG ACCCGGGCGA GCCGATCGCG	3240
ATCGTGGGGA TGGCCTCCCG CCTGCCGGGT GCGGTGGCGT CCCCGBAAGA CCTGTGGCGG	3300
CTGCTGGCCG AGCGCGTCGA CGCCGTTTCG GAGTTCCCCG GCGACCGCGG CTGGGACCTG	3360
GACAGCCTGA TCGACCCGGA CCGGGAGCGC GCCGGGACGT CGTACGTCGG CCAGGGCGGA	3420
TTCTGACAG ACGCCGGCGA GTTCGACGCC GGGTTCTTCG GGATCTCGCC GCGTGAGGCC	3480
GTCGCGATGG ACCCGCAGCA GCGGTTGCTG CTGGAGACGT CGTGGGAGGC CCTCGAAAAC	3540
GCCGGAGTCG ACCCGATCGC GTTGAAGGGC ACCGACACCG GCGTGTTCTC CGGCCTCATG	3600
GGCCAGGGGT ACGGGTCCGG CGCGGTGGCG CCGGAGCTCG AAGGTTTCGT CACCACCGGG	3660
GTCGCGTCGA GCGTGGCCTC GGGCCGGGTG TCGTACGTGC TGGGACTGGA AGGCCCGGCG	3720

GTCACCGTGG ACACCGCGTG TTCGTCGTG CTGGTCGCGA TGCACCTGGC CGCGCAGGCC 3780

CTGCGGCAGG GCGAATGCTC GATGGCGCTC GCCGCGGGG TCACGGTGAT GGCCACGCCG 3840

GGCTCGTTTC TCGAGTTCTC CCGCCAGCGG GCCCTGGCGC CCGACGGGCG CTGCAAGGCC 3900

TTCGCGGCGG CGGCCGACGG GACCGGCTGG TCCGAGGGTG TCGGCGTGGT CGTCCTCGAG 3960

CGGCTGTCCG TGGCGCGCGA GCGGGGCCAC CGGATCCTGG CCGTTTTGCG TGGCAGCGCG 4020

GTCAACCAGG ACGGCGCGTC CAACGGGCTC ACCGCGCCGA ACGGCCTCTC GCAGCAGCGG 4080

GTCATCCGCC GCGCGCTGGC CGCGGCCGGG CTGGCACCGT CCGATGTGGA CGTCGTCGAG 4140

GCGCACGGCA CCGGGACCAC GCTGGGTGAC CCGATCGAGG CGCAGGCCCT GCTGGCGACC 4200

TACGGCCAGG AGCGGAAGCA GCCGTTGTGG CTCGGTTCGC TCAAGTCGAA CATCGGCCAC 4260

GCGCAGGCGG CCGCGGGCGT TCGGGGCGTC ATCAAGATGG TGCAGGCGCT GCGGCACGAG 4320

ACCTTGCCGC CGACGCTGCA TGTCGACAAG CCGACTCTTG AGGTGGACTG GTCCGCCGGT 4380

GCCATTGAAC TGCTGACGGA GGCCCGTGCG TGGCCGCGCA ACGGCCGTCC GCGCCGGGCC 4440

GGGGTGTGCT CGTTCGGCGT CAGCGGGACC AACGCGCACC TGATCCTGGA GGAGGCGCCG 4500

GCCGAGGAGC CGGTCGCTGC CCCGGAAGTG CCGGTGGTGC CCCTGGTGGT GTCGGCGCGG 4560

AGCACGGAGT CGCTGTCCGG GCAGGCCGAG CGGCTGGCGT CCCTCCTCGA AGGGGACGTC 4620

TCGCTGACCG AGGTGGCCGG GGCGCTGGTG TCCCGCCGGG CCGTGCTGGA CGAGCGGGCC 4680

GTCGTCGTGG CCGGTTGCGG CGAGGAAGCC GTGACCGGGC TCGGGGCGCT GAACACGGCC 4740

GGTTCGGGGA CGCCGGGCAA GGTCGTGTGG GTGTTCCCGG GGCAGGGGAC GCAGTGGGCC 4800

GGGATGGGCC	GTGAGCTGCT	GGCCGAGTCC	CCGGTGTTTCG	CCGAGCGGAT	CGCCGAGTGC	4860
GCGGCCGCGT	TGGCGCCGTG	GATCGACTGG	TCGCTCGTCG	ACGTCCTGCG	CGGCGAGGGC	4920
GACCTGGGTC	GGGTCGATGT	GCTGCAGCCG	GCCTGTTTCG	CGGTGATGGT	CGGGCTGGCT	4980
GCCGTCTGGG	AGTCCGTGGG	GGTCCGGCCG	GACGCCGTCG	TCGGGCACTC	GCAGGGTGAG	5040
ATCGCGGCTG	CCTGCGTTTC	GGGGGCGTTG	TCCCTCGAGG	ACGCGGCGAA	GGTGGTGGCC	5100
CTGCGCAGCC	AGGCCATCGC	GGCGGAACTG	TCCGGCCGCG	GCGGGATGGC	GTCGGTCGCC	5160
CTGGGCGAGG	ACGACGTCGT	TTCGCGGCTG	GTGGACGGGG	TCGAGGTCGC	CGCCGTCAAC	5220
GGCCCGTCGT	CGGTGGTGAT	CGCCGGGGAT	GCCCATGCCC	TCGACGCGAC	CCTGGAAATC	5280
TTGTCCGGGG	AAGGCATCCG	GGTTCGGCGG	GTGGCGGTGG	ACTACGCCTC	GCACACCCGG	5340
CATGTCGAGG	ACATCCGCGA	CACTCTTGCC	GAAACCTTGG	CCGGGATCAG	TGCGCAGGCG	5400
CCGGCTGTGC	CGTTCTACTC	CACCGTCACG	AGCGAGTGGG	TGCGCGACGC	GGGGGTGCTG	5460
GACGGCGGCT	ACTGGTACCG	GAACCTGCGC	AACCAGGTCC	GGTTCGGAGC	GGCCGCGACG	5520
GCCCTGCTCG	AGCAGGGCCA	CACGGTGTTT	GTCCAGGTCA	GTGCGCACCC	GGTGACGGTC	5580
CAGCCCTTGA	GCGAGCTCAC	CGGGGACGCG	ATCGGGACAT	TGCGGCGTGA	AGACGGTGGC	5640
CTGCGGCGGT	TGCTGGCTTC	GATGGGTGAG	CTGTTCTGTC	GCGGCATCGA	CGTEGACTGG	5700
ACGGCGATGG	TGCCCCGCGC	CGGCTGGGTC	GACTTGCCGA	CCTACGCGTT	CGAACACCGG	5760
CACTACTGGC	TCGAGCCCGC	CGAGCCCGCT	TCGGCCGGAG	ACCCGCTGCT	GGGCACAGTC	5820
GTCAGCACTC	CCGGTTCGGA	CCGACTCACC	GCCGTGGCGC	AGTGGTCGCG	CCGGGCGCAG	5880
CCCTGGGCGG	TGGACGGCCT	GGTGCCGAAC	GCGGCCCTGG	TCGAGGCGGC	CATCCGGCTC	5940

GGCGACCTGG CCGGCACCCC CGTCGTCGGC GAACTGGTCG TCGACGCGCC GGTGGTGCTG 6000

CCGCGGCGCG GCAGCCGCGA GGTCCAGCTG ATCGTCGGCG AGCCCGGCGA GCAGCGGCGG 6060

CGTCCGATCG AGGTCTTTTC CCGGGAAGCC GACGAGCCGT GGACCGGCA CGCGCACGGC 6120

ACACTCGCTC CCGCCGCCGC TCGGGTGCCA GAACCGGCGG CGGCGGGAGA CGCCACCGAC 6180

GTCACCGTGG CCGGCCTGCG CGACCGGAC CGGTACGGGA TCCACCCCGC GCTGCTGGAC 6240

GCCGCCGTCC GCACGGTCGT CGGCGACGAC CTGCTCCCGT CGGTGTGGAC CGGCGTGTCC 6300

CTGCTGGCCT CCGGGGCCAC GGCCGTGACC GTGACGCCGA CGGCGACCGG CCTGCGGCTG 6360

ACCGACCCGG CCGGGCAGCC CGTCCTGACC GTCGAATCCG TCGCGCGCAC GCCGTTCGTC 6420

GCCGAGCAGG GGACCACCGA CGCGCTCTTC CGCGTCGACT GGCCGGAAAT CCCGCTGCCC 6480

ACCGCCGAAA CCGCGGACTT CCTGCCGTAC GAAGCCACGT CGGCCGAGGC GACCCCTCTCC 6540

GCGCTCCAGG CCTGGCTGGC AGACCCCGCG GAAACCCGGC TGGCCGTGGT CACCGGGGAC 6600

TGCACCGAAC CCGGCGCGGC CGCGATCTGG GGCCTGGTGC GCTCGGCGCA GTCCGAACAC 6660

CCCGGCCGGA TCGTGCTGGC CGACCTCGAC GACCCCGCCG TGCTGCCCCG CGTGGTGGCG 6720

AGCGGCGAAC CGCAGGTGCG GGTGCGCAAC GGCCTGCCTT CGGTGCCGCG CTTGACCCGG 6780

GTTACTCCCC GGCAGGACGC GCGGCCGCTC GACCCCGAGG GCACCGTCCT GATCACCGGC 6840

GGCACC GGCA CGCTCGGTGC GCTGACCGCC CGGCACCTCG TCACCGCGCA CGGCGTCCGG 6900

CACCTGGTGC TGGTCAGCCG CCGCGGTGAG GCTCCCGAGC TGCAGGAAGA ACTGACCGCA 6960

CTGGGGGCAT CCGTCGCCAT CGCCGCCTGC GACGTGGCAG ACCGGGCGCA GCTCGAAGCC 7020

20250505 15:46:00

GTCTTGCGCG CGATCCCGGC CGAGCACCCG CTCACCGCCG TGATCCACAC CGCGGGGGTC 7080

CTCGACGACG GCGTCGTAC CGAGCTGACC CCGGACCGGC TCGCCACCGT GCGGCGGCCG 7140

AAGGTCGACG CCGCCCGGCT CCTGGACGAG CTCACCCGGG AGGCCGATCT CGCCCGGTTT 7200

GTGCTGTTCT CCTCGGCGGC GGGTGTGCTG GGCAACCCCG GCCAGGCCGG GTACGCCGCC 7260

GCCAACGCCG AGCTGGATGC GTTGGCGCGC CAGCGGAACA GCCTCGACCT GCCC CGGTG 7320

TCCATCGCAT GGGGCTACTG GGCGACGGTC AGCGGGATGA CCGAGCACCT GGGCGACGCC 7380

GACCTGCGGC GCAACCAGCG GATCGGCATG TCCGGGCTTC CCGCCGACGA GGGCATGGCG 7440

CTGCTGGACG CCGCCATCGC CACCGGTGGC ACGCTGGTCG CGGCCAAGTT CGACGTCGCC 7500

GCGCTGCGGG CGACGGCGAA GGCCGGCGGC CCGGTGCCGC CGCTGCTGCG TGGCCTGGCC 7560

CCGCTGCCGC GCCGGGCGGC GGCCAAGACC GCGTCGCTGA CCGAACGCCT CGCCGGGCTG 7620

GCCGAGACCG AGCAGGCCGC GGCCCTGCTC GACCTGGTCC GGCGGCACGC CGCCGAGGTG 7680

CTCGGGCACA GCGGCGCCGA ATCCGTCCAT TCAGGACGGA CGTTCAAGGA CGCCGGCTTC 7740

GA CTCGCTGA CCGCGGTGGA ACTGCGGAAC CGCCTCGCGG CCGCGACCGG GCTCACCCTG 7800

TCCCCGGCGA TGATCTTCGA CTACCCGAAG CCCCCGGCGC TCGCGGACCA CCTGCGCGCC 7860

AAGCTCTTCG GATCGGCGGC GAACCGGCCG GCCGAGATCG GCACCGCCGC GGCCGAGGAG 7920

CCGATCGCGA TCGTCGCGAT GGCGTGCCGC TTCCCCGGTG GCGTGACAG CCCCAGGAC 7980

CTGTGGCGGC TGGTCGCCGA CGGCGCCGAC GCCGTACCG AGTTCCCCGC CGACCGCGGC 8040

TGGGACACCG ACCGGCTCTA CCACGAAGAC CCCGACCAG AAGGCACGAC GTACGTCCGG 8100

CACGGCGCCT TCCTCGACGA CGCCGCCGGG TTCGACCCG CCTTCTTCGG CATCTCGCCG 8160

CGCGGGGGTC

AACGAGGCGC TCGCCATGGA CCCGCAGCAG CGGCTGCTGC TGGAGACGTC CTGGGAGCTG 8220

TTCGAGCGGG CCGCGATCGA CCCGACCACG CTGGCCGGCC AGGACATCGG CGTCTTCGCC 8280

GGCGTCAACA GCCACGACTA CAGCATGCGG ATGCACCGGG CCGCCGGTGT CGAGGGCTTC 8340

CGECTCACCG GCGGTTCGGC CAGCGTGCTC TCCGGCCGCG TCGCCTACCA CTTCGGCGTC 8400

GAAGGCCCCG CCGTCACGGT CGACACGGCC TGCTCGTCTT CGCTGGTCGC GCTGCACATG 8460

GCGGTGCAGG CCCTGCAGCG CGGCGAGTGC TCCATGGCGC TCGCGGGCGG CGTGATGGTG 8520

ATGGGCACGG TCGAGACGTT CGTCGAGTTC TCGCGGCAGC GCGGGCTGGC CCCCACGGC 8580

CGCTGCAAGG CGTTCGCCGA CGGCGCGGAC GGCACCGCT GGTCCGAGGG CGTCGGGCTG 8640

CTCCTGGTGG AGCGGCTGTC CGAGGCTCAG CGTCGCGGGC ACCAGGTCCT CGCCGTGGTC 8700

CGCGGGTCGG CGGTCAACTC CGACGGCGCG TCGAACGECT TGACGGCCCC GAACGGCCCCG 8760

TCCCAGCAGC GCGTGATCCG CAAGGCACTG GCCGCCGCCG GACTGTCCAC ATCGGACGTC 8820

GACGCGGTGG AGGCGCACGG CACCGGGACG ACCCTGGGCG ACCCGATCGA GGCCGAGGCG 8880

CTGCTGGCCA CCTACGGCCA GAACGGGAA ACGCCGCTGT GGCTCGGCTC GGTGAAGTCG 8940

AACCTCGGGC ACACGCAGGC GGCTGCGGGT GTCGCAGGCG TGATCAAGAT GGTCAATGGCC 9000

ATGCGCCACG GCGTCCTGCC CCGGACGCTG CACGTCGACC GGCCGTCGTC CTATGTGGAC 9060

TGGTCGGCCG GTGCGGTCEA GCTGCTGACC GAGGCACGGG ACTGGGTGAG CAACGGCCAC 9120

CCGCGCCGCG CGGGCGTGTC GTCGTTCCGG ATCGGCGGCA CCAACGCGCA CGTCGTCCTC 9180

GAAGAGGTTG CCGCACCGAT CACCACGCCG CAGCCTGAGC CGGCCGAGTT CCTGGTGCCG 9240

GTGCTCGTCT	CCGCGCGGAC	GGCGGCGGGT	CTGCGCGGCC	AGGCCGGACG	GCTCGCCGCG	9300
TTCTTCGGCG	ACCGGACCGA	CGTCCGCGTC	CCCGATGCCG	CCTACGCACT	GGCCACCACG	9360
CGCGCCCAGC	TCGACCACCG	GGCCGTCGTC	CTGGCCTCCG	ACCGGGCACA	GCTCTGCGCG	9420
GACCTTGCCG	CGTTCGGCTC	CGGCGTCGTG	ACCGGAACGC	CGGTTGACGG	CAAGCTGGCC	9480
GTGCTCTTCA	CCGGCCAGGG	CAGCCAGTGG	GCCGGGATGG	GCCGTGAACT	CGCCGAGACG	9540
TTCCCGGTCT	TCCGCGACGC	CTTCGAGGCC	GCGTGCGAGG	CCGTGGACAC	GCACCTGCGT	9600
GAGCGTCCGC	TGCGCGAGGT	CGTGTTTCGAC	GACAGCGCGC	TGCTCGACCA	GACGATGTAC	9660
ACCCAGGGCG	CCCTGTTCGC	CGTGGAGACC	GCCTTGTTCC	GGCTCTTCGA	GTCCTGGGGT	9720
GTGCGGCCCG	GTCTCCTCGC	CGGTCACTCG	ATCGGCGAGC	TCGCCGCCGC	GCACGTGTCC	9780
GGCGTGCTGG	ACCTGGCCGA	CGCGGGCGAG	CTGGTCGCCG	CGCGCGGCCG	GCTGATGCAG	9840
GCCCTGCCCC	CGGGCGGCGC	GATGGTCGCC	GTCCAGGCGA	CCGAGGACGA	AGTCGCGCCC	9900
CTGCTCGACG	GCACGGTCTG	CGTCGCCCGG	GTCAACGGTC	CGGACTCGGT	GGTGCTCTCC	9960
GGCACCGAAG	CCGCCGTGCT	CGCCGTGCGG	GATGAACTGG	CTGGTCGCGG	CCGTAAGACC	10020
CGACGGCTGG	CCGTGAGCCA	CGCCTTCCAC	TCGCCGCTCA	TGGAACCGAT	GCTCGACGAC	10080
TTCCGCGCGG	TCGCCGAACG	CCTGACGTAC	CGGGCCGGTT	CGCTGCCCGT	CGTCTCGACG	10140
CTGACCGGGG	AACTCGCGGC	GCTCGACAGC	CCGGACTACT	GGGTCGGCCA	GGTGCGCAAC	10200
GCCGTGCGGT	TCAGCGACGC	CGTCACCGCG	CTGGGCGCCC	AAGGCGCGTC	GACGTTCTCT	10260
GAGCTCGGCC	CGGGCGGTGC	GCTCGCCCGG	ATGGCGCTCG	GCACGCTCGG	CGGACCCGAG	10320
CAGAGCTGCG	TCGCGACCCT	GCGCAAGAAC	GGCGCCGAGG	TGCCCCACGT	CCTCACC GCG	10380

CTCGCCGAAC TGCACGTCCG GGGCGTGGGC GTCGACTGGA CGACCGTGCT CGACGAACCG 10440

GCCACGGCGG TCGGGACCGT CCTGCCCACC TACGCGTTCC AGCACCAGCG CTTCTGGGTC 10500

GACGTCGACG AAACAGCGGC CGTCAGCGTC ACCCCGCCGC CGGCGGAGCC GATCGTGGAC 10560

CGGCCGGTGC AGGACGTGCT GGAGCTGGTC CGGGAGAGCG CCGCGGTGGT GCTCGGGCAC 10620

CGGGACGCCG GCAGTTTCGA CCTCGACCGG TCCTTCAAGG ACCACGGCTT CGACTCGCTC 10680

AGCCCGGTCA AGCTGCGCAA CCGTCTGCGC GACTTCACCG GCGTGGAGCT GCCCAGCACC 10740

CTGATCTTCG ACTACCCGAA CCCGGCCGTC CTCGCGGACC ACCTGCGGGC CGAACTGCTC 10800

GGCGAGCGCC CGGCCGCGCC GGCCCCGGTG ACGAGGGACG TCTCCGACGA GCCGATCGCG 10860

ATCGTCGGCA TGAGCACCCG GCTGCCGGGT GCGCCGACA GCCCCGAAGA GCTGTGGAAG 10920

CTCGTCGCGG AGGGACGGGA CGCCGTGTCC GGCTTCCCCG TCGACCGCGG CTGGGACCTC 10980

GACGGCCTCT ACCACCCGGA CCCC GCCCAC GCCGGGACGA GCTACACGCG TTCGGGCGGC 11040

TTCCTGCACG ACGCGGCCCA GTTCGACGCC GGGCTCTTCG GGATCTCACC GCGTGAGGCC 11100

CTGGCCATGG ACCCGCAGCA GCGGCTGCTG CTGGAGACGT CGTGGGAAGC CTTGGAGCGC 11160

GCGGGGGTCG ACCCGCTGTC CGCCCGCGGC AGCGACGTG GCGTCTTCAC CGGGATCGTC 11220

CACCACGACT ACGTGACGCG GCTGCGCGAA GTGCCCCAAG ACGTCCAGGG CTACACGATG 11280

ACCGGCACGG CTTTCGAGCGT GCGGTCGGGC CGGGTGGCGT ACGTCTTCGG CTTTCGAGGGC 11340

CCGGCGGTCA CCGTGGACAC CGCGTGTTTCG TCGTCGCTGG TCGCGATGCA CCTGGCGGCG 11400

CAGGCGCTGC GGCAGGGGGA GTGCTCGATG GCCCTGGCCG GCGGCGCGAC CGTGATGGCC 11460

AGCCCCGGACG	CCTTCCTCGA	GTTCTCCCCG	CAGCGCGGCC	TGTCCGCGGA	CGGCCGGTGC	11520
AAGGCGTACG	CGGAAGGCGC	GGACGGCACG	GGCTGGGCCG	AGGGCGTCGG	TGTCGTCGTC	11580
CTCGAACGGC	TTTCGGTGGC	ACGCGAACGT	GGCCACCGGG	TGCTGGCGGT	CCTGCGCGGC	11640
AGCGCGGTGA	ACCAGGACGG	TGCTTCCAAC	GGCCTGACCG	CCCCGAACGG	GCCGTCGCAG	11700
CAGCGGGTGA	TCCGCGGCGC	GCTGGCGAGC	GCCGGGCTGG	CACCGTCCGA	TGTGGACGTC	11760
GTGGAGGGCC	ACGGGACCGG	GACCGCGCTG	GGTGACCCGA	TCGAGGTCCA	GGCGCTGCTG	11820
GCCACCTACG	GCCAGGAGCG	GGAACAGCCG	TTGTGGCTCG	GCTCGCTGAA	GTCGAACCTC	11880
GGGCACACGC	AGGCCGCGGC	CGGGGTCGTG	GGCGTGATCA	AGATGATCAT	GGCCATGCGC	11940
CACGGCCTCA	TGCCGGCCAC	GCTGCACGTC	GACGAGCGCA	CGAGCCAGGT	CGACTGGTCG	12000
GCCGGCGCGA	TCGAGGTGTT	GACCGAGGCC	CGGGAGTGGC	CGCGCACCGG	ACGTCCGCGC	12060
CGGGCCGGGG	TGTCCTCCTT	CGGCGCCAGC	GGCACCAACG	CGCACCTGAT	CATCGAGGAA	12120
GGTCCCGCCG	AAGAGGCCGT	GGACGAAGAG	GTGGCCTCCG	TGGTGCCGCT	GGTCGTCTCC	12180
GCCCCGACCG	CCGGTTCGCT	GGCCGGGCAG	GCCGGGCGCC	TGGCCGCGGT	CCTCGAGAAC	12240
GAATCGTTGG	CCGGGGTGGC	CGGTGCCCTG	GTTTCCGGCC	GCGCGACGCT	GAACGAGCGC	12300
GCGGTCGTCA	TCGCGGGCTC	CCGCGACGAG	GCCCAGGACG	GCCTGCAGGC	ACTGGCCCCG	12360
GGCGAGAACG	CGCCCGCGGT	CGTGACCGGG	ACGGCGGGCA	AGCCGGGCAA	GGTCGTCTGG	12420
GTCTTCCCCG	GCCAGGGCTC	GCAGTGATG	GGCATGGGCC	GGGACCTCCT	GGACTCCTCG	12480
CCGGTGTTTCG	CCGCGCGGAT	CAAGGAATGC	GCTGCGGCAC	TGGAACAGTG	GACCGACTGG	12540
TCGCTGCTGG	ACGTGCTGCG	CGGCGACGCC	GACCTGCTGG	ACCGGGTCGA	CGTGGTGCAG	12600

CCGGCCAGCT TCGCGATGAT GGTCGGGCTC GCCGCGGTGT GGACCTCGCT GGGGGTGACC 12660

CCGGATGCGG TGCTCGGCCA CTCCCAGGGC GAGATCGCCG CGGCGTGCGT GTCCGGCGCG 12720

CTGTCGCTGG ACGACGCGGC GAAGGTGGTC GCGTTGCGCA GCCAGGCGAT CGCGGGGGAG 12780

CTGGCGGGCC GCGGCGGGAT GGCGTCGGTC GCACTGAGCG AAGAGGACGC AGTCGCGCGG 12840

CTGACGCCGT GGGCGAACCG GGTCGAGGTG GCCGCGGTCA ACAGCCCGTC CTCGGTCGTC 12900

ATCGCGGGAG ACGCGCAGGC CCTCGACGAA GCCCTCGAAG CCCTGGCCGG CGACGGTGTC 12960

CGGGTCCGGC GGGTCGCGGT GGA CTACGCC TCCCACACCC GGCACGTCGA GGCGATCGCC 13020

GAAACCCTGG CCAAGACCTT GGCCGGGATC GACGCGCGGG TTCCGGCGAT TCCGTTCTAT 13080

TCCACCGTCC TGGGCACGTG GATCGAGCAG GCCGTCGTCG ACGCGGGCTA CTGGTACCGG 13140

AACCTGCGGC AGCAGGTGCG GTTCGGCCCC TCGGTGGCGG ACCTGGCCGG GCTGGGGCAC 13200

ACGGTGTTTCG TGGAGATCAG CGCCCACCCG GTGCTGGTCC AGCCGCTGAG CGAGATCAGC 13260

GACGACGCGG TEGTGACCGG GTCGCTGCGG CGGGACGACG GGGGACTGCG GCGCCTGCTG 13320

GCGTCGGCGG CCGAACTGTA CGTCCGGGGC GTGGCCGTGG ACTGGACGGC GGCCGTGCCC 13380

GCGGCCGGCT GGGTGGACCT GCCGACGTAC GCCTTCGACC GCCGCCACTT CTGGCTGCAC 13440

GAAGCCGAGA CCGCCGAAGC CGCCGAGGGC ATGGACGGCG AGTTCTGGAC GGCGATCGAA 13500

CAGTCCGATG TGGACAGCTT GGCCGAGCTG CTCGAGCTGG TGCCGGAGCA GCGCGGGGCG 13560

CTCAGCACCG TCGTGCCCGT GCTGGCGCAG TGGCGGGACC GCGCCCGCA GCGCTCGACC 13620

GCGGAGAAGC TCGGCTACCA GGTCACCTGG CAGCCCCTGG AGCGCGAAGC CGCCGGCGTG 13680

CCGGGCGGGC GCTGGCTGGC CGTCGTCCCG GCCGGCACCA CCGACGCGCT CCTGAAGGAG 13740
CTGACCGGCC AGGGACTCGA CATCGTCCGG CTGGAGATCG AGGAAGCTTC GCGGGCACAG 13800
CTCGCCGAGC AGCTGCGGAA CGTCCTGGCG GAGCACGACC TCACCGGCGT GCTGTGCGTG 13860
CTCGCTCTCG ACGGCGGGCC CGCGGACGCG GCCGAGATCA CCGCGTCGAC GCTCGCGCTG 13920
GTCCAGGCCC TGGGCGACAC CACCACGTCC GCGCCGCTGT GGTGCCTCAC TTCCGGCGCG 13980
GTGAACATCG GCATCCAGGA CGCCGTGACC GCACCGGCCC AGGCGGCCGT GTGGGGGCTC 14040
GGCCGGGCGG TCGCGCTGGA GCGCCTCGAC CGGTGGGGCG GCCTGGTCGA CTTGCCCGCC 14100
GCGATCGACG CCCCCACGGC TCAGGCCCTG CTCGGCGTCC TGAACGGCGC CGCCGGGGAA 14160
GACCAGCTCG CGGTCCGGCG CTCGGGCGTC TACCGCAGGC GGCTGGTCCG CAAGCCCGTG 14220
CCGGAGTCCG CGACGAGCCG GTGGGAACCC CGCGGCACGG TCCTGGTGAC CGGTGGGGCC 14280
GAAGGACTCG GCCGGCACGC CTCGGTCTGG CTCGCGCAGT CCGGCGCCGA ACGGCTCATC 14340
GTCACCGGCA CCGACGGCGT CGACGAACTG ACGGCCGAGC TGGCCGAGTT CGGCACCACG 14400
GTCGAGTTCT GCGCCGACAC CGACCGGGAC GCGATCGCGC AGCTGGTGGC GGA CTGGAG 14460
GTCACCGCCG TGGTGACGC CGCGGACATC GCGCAGACCA GTCCTGTCGA CGACACCGGC 14520
GTGGCCGACC TCGACGAGGT GTTCGCCGCG AAGGTGACCA CCGCGGTGTG GCTGGACCAG 14580
CTGTTGAGG ACACCCCGCT CGACGCGTTC GTCGTGTTCT CCTCGATCGC CGGCATCTGG 14640
GGCGGTGGCG GGCAGGGCCC GGCGGGTGCG GCGAACGCCG TCCTCGACGC CCTGGTCGAA 14700
TGGCGCCGGG CCCGCGGCCT CAAGGCGACG TCGATCGCCT GGGGCGCGCT CGACCAGATC 14760
GGCATCGGCA TGGACGAGGC CGCCCTCGCC CAGCTGCGCC GCCGCGGTGT CATCCCGATG 14820

20250529150400

ECGCCGCCGC TGGCGGTCAC CGCGATGGTG CAGGCGGTCTG CCGGCAACGA GAAGGCCGTG 14880

GCGGTGGCCG ACATGGACTG GGCCGCCCTTC ATCCCGGCGT TCACCTCGGT CCGGCCCAGC 14940

CCGCTGTTCG CCGATCTGCC CGAGGCGAAG GCCATCCTCC GGGCGGCGCA GGACGACGGC 15000

GAAGACGGCG ACACCGCGTC GTCGCTCGCG GACTCCCTGC GCGCGGTCCC CGACGCCGAG 15060

CAGAACCGCA TCCTGCTGAA GCTGGTCCGC GGCCACGCTT CGACGGTGCT CGGCCACAGC 15120

GGCGCCGAAG GCATCGGCCC GCGCCAGGCG TTCCAGGAGG TCGGCTTCGA CTCGCTGGCC 15180

GCGGTCAACC TCCGCAACAG CCTGCACGCG GCCACCGGGC TCGGCTGCC CGCGACGCTG 15240

ATCTTCGACT ACCCCACCCC GGAGGCGCTG GTCGGCTACC TCGCGTCGA ACTCCTGCGG 15300

GAGGCCGACG ACGGCCTGGA CGGGCGGGAA GACGACCTCC GGCGAGTCCT CGCGGCCGTG 15360

CCGTTCGCCC GGTTC AAGGA GGCGGGCGTG CTGGACACGC TGCTCGGCCT CGCCGACACC 15420

GGCACC GAAC CGGGCACGGA CGCCGAGACC ACCGAAGCGG CCCC GGCCGC CGACGACGCA 15480

GAAGTGATCG ACGCACTGGA CATCTCCGGT CTCGTGCAAC GAGCCCTCGG GCAGACGAGC 15540

TGACCGCCGA TGGCGAACCA ATCGTGAGG AAGAACATGT CCGCGCCGAA CGAGCAGATC 15600

GTTGACGCAC TCGCGCGTC GCTGAAGGAG AACGTCCGGC TTCAGCAGGA GAACAGCGCG 15660

CTCGCCGCGG CCGCCGCGGA GCCCGTCGCG ATCGTCTCCA TGGCCTGCCG CTACGCGGGC 15720

GGGATCCGCG GCCCGGAGGA CTTCTGGCGG GTGGTGTCCG AAGGCGCCGA CGTCTACACC 15780

GGCTTCCCCG AGGACCGCGG CTGGGACGTC GAAGGCCTCT ACCACCCGGA CCCC GACAAC 15840

CCCGGCACGA CGTACGTGCG GGAGGGCGCC TTCCTGCAGG ACGCGGCCCA GTTCGACGCC 15900

GGGTTCTTCG GCATCTCGCC GCGCGAGGCG CTGGCCATGG ACCCCCAGCA GCGGCAGCTC 15960

CTGGAGGTGT CCTGGGAGAC CTTGGAACGG GCCGGCATCG ACCCGCATTC GGTGCGGGGC 16020

AGCGACATCG GCGTCTACGC CGGGGTCTGT CACCAGGACT ACGCCCCCGA CCTCAGCGGG 16080

TTCGAAGGCT TCATGAGCCT GGAGCGCGCC CTGGGCACCG CGGGCGGTGT CGCCTCCGGC 16140

CGGGTCGCCT ACACGCTCGG GCTCGAAGGC CCCGCCGTCA CCGTCGACAC GATGTGCTCG 16200

TCGTCGCTGG TGGCGATTCA CCTTGCCGCG CAAGCTCTTC GCCGTGGTGA GTGCTCGATG 16260

GCCCTCGCGG GCGGCTCGAC CGTGATGGCG ACCCCGGGCG GGTTCGTCGG CTTCGCGCGT 16320

CAGCGGGCGT TGGCCTTCGA CGGGCGCTGC AAGTCTTACG CCGCGGCCGC CGACGGTTCC 16380

GGCTGGGCCG AGGGCGTCGG CGTGCTGCTG CTGGAGCGGC TGTCGGTGGC GCGCGAGCGC 16440

GGGCACCAGG TGCTGGCCGT CATCCGCGGC AGCGCGGTCA ACCAGGACGG CGCTTCCAAC 16500

GGCCTGACCG CGCCCAACGG CCCGGCGCAG CAGCGGGTCA TCCGCAAGGC ACTGGCGAGC 16560

GCCGGGCTGA CACCGTCCGA TGTGGACACC GTGGAGGGCC ACGGCACCGG CACCGTCTC 16620

GGCGACCCGA TCGAGGTCCA GCGCTGCTG GCCACCTACG GCCAGGGCCG CGACCCGCAG 16680

CAACCGCTGT GGCTGGGCTC GGTCAAGTCC GTCGTCGGGC ACACGCAGGC GGCATCCGGT 16740

GTGGCCGGCG TGATCAAGAT GGTCCAGTCG CTGCGGCACG GGCAGTCCC GGCGACCCAG 16800

CACGTCGACG CGCCACGCC GCAAGTGGAC TGGTCGGCCG GAGCGATCGA GCTGCTGGCC 16860

GAGGGCCGGG AGTGGCCGCG CAACGGCCAC CCGCGCCGGG GCGGCATCTC GTCGTTCCGG 16920

GCCAGCGGCA CGAACGCGCA CATGATCCTC GAAGAAGCGC CCGAGGACGA GCCGGTGACC 16980

GAAGCGCCGG CGCCACGGG TGTGCTACCG CTGGTGGTGT CGGCGGCGAC CGCTGCTTCC 17040

CTGGCCGCCC AGGCCGGTCG GCTGGCGGAG GTCGGCGACG TCTCCCTGGC GGATGTCGCC 17100

GGGACGCTGG TGTCCGGCCG CGCGATGCTC AGCGAGCGCG CGGTCGTCGT GGCCGGCTCC 17160

CACGAAGAAG CCGTGACCGG GCTGCGGGCG CTGGCCCGCG GCGAGAGCGC GCCCGGCCTG 17220

CTTTCCGGCC GCGGCTCGGG GGTCCCGGGC AAGGTCGTCT GGGTGTTCCT CGGCCAGGGC 17280

ACGCAGTGGG CCGGCATGGG CCGCGAGCTG CTGGACTCCT CGGAGGTGTT CGCCGCGCGG 17340

ATCGCCGAGT GCGAGACCGC GCTCGGGCGG TGGGTGCGACT GGTGCTGAC CGACGTGCTG 17400

CGCGGCGAGG CCGACCTGCT GGACCGGGTC GACGTGGTGC AACCGGCGAG CTTCGCCGTG 17460

ATGGTCGGGC TTGCCGCCGT CTGGGCCTCC CTCGGCGTCG AGCCCGAGGC CGTGGTGGGC 17520

CACTCGCAGG GCGAGATCGC GGCCGCATGC GTGTCCGGG CACTGTCCCT GGAGGACGCG 17580

CGGAAGGTGG TGGCGTTGCG CAGCCAGGCG ATCGCCGCCT CGCTGGCCGG CCGGGGCGGC 17640

ATGGCGTCGG TCGCGTTGAG CGAAGAAGAC GCGACCGCGC GGCTCGAGCC GTGGGCGGGC 17700

CGCCTGGAGG TCGCCGCCGT CAACGGGCCG ACGTCCGTGG TGATCGCCGG GGACCCGAG 17760

GCGCTGGACG AAGCCCTCGA CGCGCTCGAC GACCAAGGCG TCCGGATCCG GCGGGTGGCG 17820

GTGGACTACG CCTCCACAC CCGGCACGTC GAAGCCGCGC GCGACGCACT GGCCGAGATG 17880

CTGGGCGGGA TCCGCGCGCA GGCGCCGGAA GTGCCGTTCT ACTCGACCGT GACCGGCGGC 17940

TEGGTCGAAG ACGCCGGCGT GCTCGACGGC GGCTACTGET ACCGGAACCT CCGCCGTCAG 18000

GTGCGGTTCTG GCCCGGCGGT GGCCGAGCTG ATCGAGCAGG GCCACCGGGT GTTCGTGAG 18060

GTCAGCGCGC ATCCCGTCT GTTTCAGCCG ATCAACGAAC TCGTCGACGA CACCGAAGCC 18120

GTGGTCACCG GGACGCTGCG GCGCGAGGAC GCGGGCCTCC GCGCCTGCT GGCCTCGGCG 18180

GCCGAGCTCT TCGTCCGCGG CGTGACCGTG GACTGGTCCG GTGTGCTGCC ACCGTCCCGC 18240

CGGGTCGAGC TGCCGACGTA CGCCTTCGAC CACCAGCACT ACTGGCTGCA GATGGGCGGG 18300

TCGGCCACCG ACGCCGTGTC GCTGGGCCTG GCCGGCGCCG ACCACCCGCT GCTGGGCGCG 18360

GTCGTCCCGC TGCCGCAGTC CGACGGGCTC GTCTTCACCT CGCGGCTGTC GCTGAAGTCG 18420

CACCCGTGGC TGGCCGGGCA CGCGATCGGC GGGGTCGTGC TCATTCCGGG CACGGTGTAC 18480

GTCGACCTCG CGCTGCGCGC CGGCGACGAG CTCGGCTTCG GCGTCCTGGA AGAGCTCGTG 18540

ATCGAGGCAC CGCTGGTGCT GGGCGAGCGC GCGGGCGTTC GCGTGCAGGT CGCCGTGAGC 18600

GGGCCGAACG AGACCGGCTC GCGTCCGGTG GACGTCTTCT CCATGCGGGA AGACGGCCAC 18660

GAATGGACCC GGCACGCGAC CGGTCTCCTC GGGGCGTCGA CGTCCCGGGA ACCGAGCCGC 18720

TTCGACTTCG CCGCCTGGCC GCCGGCCGGG GCGGAGCCGA TCGACGTCGA AAACCTCTAC 18780

ACCGACCTCA CCGAGCGCGG GTACGCCTAC AGCGGCGCCT TCCAGGGCAT GCGGGCGGTC 18840

TGGCGGCGCG GTGACGAGGT CTTCGCCGAG GTCGCGCTGC CTGACGACCA CCGCGAGGAC 18900

GCCGGCAAGT TCGGCCTCCA CCCC GCCCTC CTCGACGCCG CTCTGCACAC GAACGCCTTC 18960

GCGAACCCGG ACGACGACCG CAGTGTGCTG CCGTTCGCGT GGAACGGCCT GGTCTCTGCAC 19020

GCCGTGGGCG CGTCGGCGCT GCGGGTGCGG GTGGCGCCGG GCGGTCCGGA CGCGCTGACG 19080

TTCCAGGCCG CCGACGAGAC CGGTGGCCTG GTCGTCACCA TGGATTGCTT GGTGTCCCGC 19140

GAGGTGTGCG CCGCGCAGCT GGAGACGGCG GCGGGCGAAG AGCGCGACTC GCTGTTCCAG 19200

GTGGA CTGGA TCGAGGTCCC CGCGACCGAG ACCGCGGCCA CCGAGCACGC CGAGGTGCTC 19260

GAAGCCTTCG GCGAGGCAGC GCCCCTCGAG CTGACCAGCC GGGTGCTGGA GGCCGTGCAG	19320
TCCTGGCTCG CCGACGCGGC CGACGAAGCA CGGTTGGTCG TGGTGACCCG TGGCGCCGTG	19380
CGCGAGGTGA CGGACCCGGC CGGTGCCGCC GTGTGGGGTT TGGTGCGAGC CGCCCAGGCG	19440
GAGAACCCGG GCCGGATCAT CCTCGTCGAC ACCGACGGCG ACGTCCCGCT GGGTGCGGTG	19500
CTGGCCAGTG GTGAGCCGCA GCTCGCCGTG CGCGCAACG CTTTCTCCGT CCCGCGCCTC	19560
GCCCGGGCCA CCGGCGAGGT GCCGGAGGCC CCCGCGGTGT TCAGTCCGGA AGGGACGGTC	19620
CTGCTCACCG GCGGCACCGG CTCGCTGGGC GGTCTGGTGG CCAAGCACCT GGTGCCCCGG	19680
CACGGCGTCC GCGGCTGGT GCTCGCCAGC CGCCGAGGCG TGGCCGCGGA AGACCTCGTC	19740
ACCGAGCTGA CCGAGCAGGG CGCGACCGTG TCCGTGGTGG CTTGCGACGT CTCCGACCGC	19800
GACCAGGTGG CCGCGTTGCT GGCCGAACAC CGCCCGACCG GCATCGTGCA CCTGGCCGGC	19860
CTGCTGGACG ACGGCGTCAT CGGAGCCCTG AACCAGGAGC GGCTGGCCGG GGTGTTGCG	19920
CCCAAGGTCG ATGCCGTCCA GCACCTCGAC GAACTGACCC GCGACCTCGG CCTCGACGCG	19980
TTGCTCGTGT TCTCGTCCGC AGCCGCGCTC ATGGGCTCCG CCGGCCAGGG CAACTACGCG	20040
GCCGCCAACG CCTTCTCGA CGGCTTGATG GCCGGGCGCC GCGCGGCGGG CCTGCCAGGC	20100
GTGTCCCTGG CGTGGGGCCT GTGGGAGCAG GCGGACGGCC TGACCGCGAA CCTCAGCGCC	20160
ACCGACCAGG CCCGGATGAG CCGCGGCGGC GTGCTGCCGA TGACACCGGC CGAGGCCCTG	20220
GACATCTTCG ACATCGGCCT GGCCGCCGAG CAGGCCCTGC TGGTCCCGAT CAAGCTCGAC	20280
CTGCGGACGC TGC GCGGCCA GGCCACCGCC GCGGCGAGG TGCCGCACCT GCTGCGCGGC	20340

CTGGTCCGCG CGAGCCGCCG CGTGACCCGC ACGGCTGCCG CGAGTGGCGG CGGTGGCCTG 20400

GTCCACAAGC TCGCCGGGCG GCCAGCCGAA GAGCAGGAAG CCGTGCTGCT GGGCATCGTC 20460

CAGGCGGAGG CGGCCGCGGT GCTCGGCTTC AACGCCCCCG AGCTGGCCCA GGGCACCCGC 20520

GGGTTACAGC ACCTCGGCTT CGACTCGCTG ACCGCGGTG AGCTGCGGAA CCGGCTGAGC 20580

GCGGCGACCG GCGTCAAATT GCCCGCCACG CTCGTCTTCG ACTACCCGAC GCCGGTCGCG 20640

CTCGCCCGCC ACCTGCGCGA AGAGCTGGGC GAGACGGTGG CGGGTGCGCC GGCCACGCCG 20700

GTGACGACCG TCGCCGACGC GGGCGAGCCG ATCGCCATCG TCGGCATGGC GTGCCGCCTG 20760

CCGGGCGGCG TGATGAGCCC CGACGACCTC TGGCGGATGG TCGCCGAGGG CCGCGATGGG 20820

ATGTCGCCGT TCCCCGAGA CCGCGGCTGG GACCTGGACG GCCTGPTCGA CTCGGACCCC 20880

GAGCGCCCGG GCACCGCCTA CATCCGCCAA GSCGGCTTCC TGCACGAGGC CGCGCTGTTC 20940

GACCCGGGCT TCTTCGGGAT CTCGCCGCGC GAAGCCCTGG CCATGGACCC GCAGCAGCGG 21000

CTGCTECTCG AAGCCTCCTG GGAAGCCCTG GAGCGCGCGG GCATCGACCC GACCAAGGCC 21060

CGCGGTGACG CCGTCGGCGT CTTCTCCGGC GTCTCCATCC ACGACTACCT CGAGTCCCTG 21120

AGCAACATCC CCGCCGAGCT CGAAGGCTTC GTCACCACGG CCACGGCGGG CAGCGTCGCC 21180

TCGGGCCGGG TGTCTACAC CTTTCGGGTTT GAGGGCCCCG CGGTACCGGT GGACACGGCG 21240

TGCTCGTCGT CGCTGGTCGC GATCCACCTG GCCGCACAGG CACTGCGGCA GGGCGAGTGC 21300

ACGATGSCC TGGCCGGCGG TGTGCGCGTG ATGGGCTCGC CGATCGGTGT CATCGGCATG 21360

TCGCGGCAGC GCGGCATGGC CGAGGACGGC CGGGTCAAGG CGTTCGCCGA CGGCGCGGAC 21420

GGCACCGTCC TGTCCGAAG CGTCGGCATC GTCGTCCTCG AACGGCTTTC GGTGGCCCCG 21480

GAACGCGGGC ACCGGGTGCT CGCCGTGCTC CGCGGCAGCG CGGTCAACCA GGACGGCGCT 21540

TCGAACGGCC TGACCGCGCC CAACGGGCCG TCGCAGCAGC GGGTGATCCG CAGCGCGCTG 21600

GCCGGGGCCG GACTGCAACC GTCCGAAGTG GACGTCTGTC AAGCGCACGG CACCGGGACC 21660

GCGCTGGGCG AACCGATCGA AGCCCAGGCC CTGCTGGCCA CCTACGGCAA GAGCCGCGAG 21720

ACGCCGTTGT GGCTCGGGTC GCTGAAGTCG AACATCGGCC ACACCCAGGC GGCCGCGGGC 21780

GTGGCGGCCG TGATCAAGAT GGTCCAGGCG CTGCGGCAGG ACACCCTGCC GCCGACCCTC 21840

CACGTGCAGG AACCACCAAA GCAGGTGGAC TGGTCCGCGG GTGCGGTCTGA GCTGCTGACC 21900

GAAGGCCGGG AGTGGGCCCC CAACGGCCAC CCGCGCCGGG CCGGTGTCTC GTCGTTCCGG 21960

ATCAGCGGCA CCAACGCGCA CCTCATCCTG GAAGAGGCGC CCGCCGACGA CACCGCCGAG 22020

GCGGACGTGC CCGACGCCGT GGTGCCCCGTG GTGATCTCCG CGCGCAGCAC CGGATCCCTG 22080

GCGGGCCAGG CCGGACGCCT GGCGGCGTTC CTCGACGGAG ACGTCCCCTG GACCCGCGTG 22140

GCGGGTGCCC TGCTGTCTGAC CCGGGCGACG CTGACCGACC GGGCCGTCGT CGTGCGGGC 22200

TCGCCCAGG AGGCCCCGGC GGGGCTGACC GCGCTGGCCC GCGCGAGAG CGCGAGCGG 22260

CTTGTAACCG GTACCGCAGG GATGCCGGGC AAGACGGTCT GGGTGTTCCC CGGCCAGGG 22320

ACGCAGTGGG CGGGCATGGG CCGGGAGCTC CTCGAAGCGT CCCCAGTGTT CGCCGAGCGC 22380

ATTGAGGAAT GCGCGGCCGC GCTGCAGCCG TGGATCGACT GGTCGCTGCT GGACGTCTCT 22440

CGTGCGGAAG GTGAGCTGGA TCGGGTCGAC GTGCTGCAGC CGGCGTGTTT CGCGGTGATG 22500

GTGGGGCTGG CCGCCGTCTG GGCCTCGGTC GCGTCGTGC CGGACGCGGT CCTGGGCCAC 22560

20250924 10:44:54

TCCCAGGGCG AGATTGCCGC CGCCTGCGTG TCGGGTGCAC TGTCCCTCGA GGACGCAGCC 22620

AAGGTGCTCG CGCTGCGCAG CCAGGCGATC GCGGCGGAGC TGTGCGGCCG CGGGGGCATG 22680

CGCTCGATCC AGCTGAGCCA CGACGAGGTG ECTGCCCCGC TCGCGCCGTG GCGGGGCCGC 22740

GTCGAGATCG CCGCCGTCAA CGGTCCGGCC TCGGTCTGTA TCGCCGGTGA CGCCGAAGCG 22800

CTCACCGAGG CCGTCAAGT CCTCGGCGGT CGGCGGGTGG CGGTGGACTA CGCGTCCCAC 22860

ACGCGGCACG TCGAGGACAT CCAGGACACC CTCGCCGAGA CTCTGGCCGG GATCGACGCG 22920

CAGGCCCCCG TGGTGCCCTT CTACTCCACG GTCGCCGGCG AGTGGATCAC CGATGCCGGG 22980

GTCGTCGACG GCGGGTACTG GTACCGGAAC CTGCGCAACC AGGTGCGCTT CGGCCCCGCC 23040

GTGCGCGAGC TGATCGAGCA GGGGCACGGG GTGTTCTGTCG AGGTCAGTGC GCATCCGGTG 23100

CTGGTGCAGC CGATCAGCGA GCTCACCGAT GCGGTCTGTA CCGGGACGTT GCGGCGCGAC 23160

GACGGTGGGG TCGGCGGGCT GCTGACCTCG ATGGCCGAAC TGTTCTGTCG CGGTGTCCCG 23220

GTCGACTGGG CCACGATGGC GCCGCCCGCG CGCGTCGAGC TGCCGACCTA CGCCTTCGAC 23280

CACCAGCACT TCTGGCTCAG CCCGCCCGCC GTGGCGGACG CGCCCGCGCT CGGCCTGGCC 23340

GGCGCCGACC ACCCGCTGCT GGGGGCGGTT CTCCCGCTGC CGCAGTCCGA CGGCCTGGTG 23400

TTCACCTCGC GCCTGTCCGT GCGGACGCAT CCGTGGCTGG CCGACGGCGT CCCC GCCGCC 23460

GCCTTGGTGG AGCTGGCCGT GCGGGCCGGT GACGAAGCCG GTTGCCCGGT CCTCGCCGAC 23520

CTEACCGTCG AAAAGCTGCT GGTGCTGCCG GAGAGCGGTG GCCTGCGCGT CCAGGTGATC 23580

GTGAGCGGCG AGCGCACGGT CGAGGTGTAT TCGCAGCTCG AAGGCGCCGA AGACTGGATC 23640

CGGAACGCCA CCGGGCACCT GTCCGCCACG GCTCCGGCGC ACGAGGCCTT CGACTTCACC 23700

CGCGTCTGTA

GCCTGGCCGC CCGCCGAGC CCAGCAGGTC GACGGCCTCT GCGGCGCGG CGACGAGATC 23760

TTCGCCGAGG TCGCCCTGCC GGAGGAGCTG GACGCCGGCG CGTTCGGCAT CCACCCCTTC 23820

CTGCTGGACG CGGCCGTGCA GCCGGTCCTC GCGGACGACG AGCAGCCGGC GGAGTGGCGC 23880

AGCCTGGTCC TGCACGCCG GGGTGCCTCG GCGCTGCGCG TCGGCTGGT GCCCCGCGGT 23940

GCCCTCCAAG CGGCGGACGA AACCGGCGGG CTGGTCCTCA CGGCGGATTC GGTGGCAGGC 24000

CGGGAActCT CGGCCGGGAA GACCCGCGCC GGATCGCTGT ACCGGGTCGA CTGGACCGAA 24060

GTGTCCATTG CAGACAGTGC GGTGCCGGCC AACATCGAGG TCGTCGAAGC CTTCCGGTGAA 24120

GAGCCCCTGG AACTGACCGG CCGGGTCCTG GAGGCTGTGC AGACCTGGCT CGTCACCGCG 24180

GCCGACGATG CGCGGCTGGT CGTGGTGACC CCGGCGCGCG TCGCGAGGT GACCGACCCC 24240

GCCGGTGCGG CCGTGTGGGG CCTGGTCCGA GCCGCGCAGG CGGAGAACCC CGGTGCGATC 24300

TTCCTGATCG ACACCGACGG CGAGATCCCG GCCCTGACCG GTGACGAGCC CGAGATCGCG 24360

GTGCGCGGCG GGAAGTTCTT CGTGCCCCGC ATCACTCGCG CGGAGCCGAG CCGGGCCGCC 24420

GTGTTCCGCC CGGACGGGAC AGTGCTGATC TCGGGCGCGG GTGCGCTCGG TGGCCTGGTG 24480

CCCCGGCGTC TCGTCGAACG CCACGGCGTG CGGAAGCTCG TGCTGGCGTC CCGGCGCGGC 24540

CGAGACGCCG ACGGCGTGGC GGACCTGGTC GCCGACCTGG CCGCGGACGT GTCCGTGGTG 24600

GCTTGCGACG TCTCCGATCG CGCCCAGGTG GCGGCCCTGC TCGACGAGCA CCGGCCGACC 24660

GCCGTGCTGC ACACCGCCGG CGTCATCGAC GCGGCGTGA TCGAGACGCT GGACCGGGAC 24720

CGGCTGGCCA CCGGTGTTGCG GCCGAAGGTC GACGCCGTGC GGCACCTCGA CGAGCTGACC 24780

CGCGACCGCG ACCTCGACGC CTTCGTCGTC TACTCCTCGG TCTCGGCCGT GTTCATGGGC 24840

GCGGGCAGCG GCAGTTACGC CGCGGCGAAC GCCTTCCTGG ACGGCCTGAT GCGGAACCGC 24900

CGGGCGGGCG GCCTGCCGGG CCTGTGCGTG GCGTGGGGCC TGTGGGACCA GAGCACCGGT 24960

ATGGCCGCCG GCACCGACGA GGCCACCCGG GCGCGGATGA GCCGCCGCCG TGGCCTGCAG 25020

ATCATGACGC AGGCCGAGGG CATGGACCTG TTCGACGCCG CGCTGTCGTC GGCCGAGTCG 25080

CTGCTGGTGC CCGCCAAGCT CGACCTGCGT GGGGTGCGCG CCGACGCCGC CGCGGGCGGG 25140

GTCGTGCCGC ACATGCTGCG TGGCCTGGTC CGCGCGGGCC GGGCGCAGGC CCGCGCGGGC 25200

TCCACTGTGG ACAACGGGCT GGCCGGACCG CTGGCCGGGC TCGCCCCGGC GGACCAGCTC 25260

ACGCTGCTCC TGGACCTGGT CCGGGCGCAG GTCGCGGCCG TGCTCGGGCA CGCCGACGCG 25320

AGCGCCGTCC GCGTCGACAC GGCTTTCAAG GACGCCGGCT TCGACTCGCT GACCGCGGTC 25380

GAGCTGCGCA ACCGCATGCG GACCGCCACC GGCTGAAGC TGCCCGCGAC GCTCGTCTTC 25440

GACTACCCGA ACCCCCAGGC GCTCGCCCGG CACCTGCGCG ACGAACTCGG TGGTGCGGCC 25500

CAGACGCCGG TGACCACAGC GGCCGCGAAG GCCGACCTCG ACGAGCCGAT CGCCATCGTC 25560

GGGATGGCGT GCCGCTTGCC GGGCGGGGTC GCCGGGCCCC AGGACCTCTG GCGECTGGTC 25620

GCCGAGGGCC GGGACGCGGT GTCGAGCTTC CCGACCGACC GCGGCTGGGA CACCGACAGC 25680

CTGTACGACC CCGATCCGGC CCGCCCGGGC AAGACCTACA CCCGGCACGG CGGCTTCCTG 25740

CACGAAGCCG GGCTCTTCGA CGCGGGCTTC TTCGGGATCT CGCCACGCGA GGCCGTCGCC 25800

ATGGACCCGC AGCAGCGGCT GCTGCTGGAG GCCTCCTGGG AGGCCATGGA AGACGCCGGG 25860

GTCGACCCAC TTTCGCTGAA GGGCAACGAC GTCGGCGTGT TCACCGGCAT GTTCGGCCAG 25920

404650400

GGTTACGTCG CTCCCGGGGA CAGCGTCGTC ACGCCGGAGC TGGAGGGTTT CGCGGGCAGC 25980

GGCGGGTCGT CGAGTGTCGC GTCCGGCCGC GTGTCTGACG TGTTCCGGTT CGAAGGCCCC 26040

GCCGTGACGA TCGACTCGGC GTGCTCGTCC TCGCTGGTCG CGATGCACCT CGCCGCGCAG 26100

TCGCTGCGGC AGGGCGAGTG CTCGATGGCC TTGGCCGGCG GCGCGACGGT GATGGCGAAC 26160

CCCGGCGCAT TCGTGGAGTT CTCGCGGCAG CGGGGCCTCG CCGTCGACGG TCGCTGCAAG 26220

GCGTTCGCCG CCGCGGCCGA CGGCACCGGC TGGGCCGAGG GCGTCGGTGT GGTTCATCTC 26280

GAGCGGCTGT CCGTGGCGCG GGAACGCGGC CACCGGATCC TGGCCGTGCT GCGCGGCAGC 26340

GCGGTCAACC AGGACGGCGC CTCGAACGGC CTGACCGCGC CGAACGGGCC GTCGCAGCAG 26400

CGGCTGATCC GCCGGGCGCT GGTGAGCGCC GGGCTGGCAC CGTCCGATGT GGACGTGTC 26460

GAGGCGCACG GCACCGGGAC CACGCTGGGT GACCCGATCG AGGCGCAAGC TCTGCTGGCT 26520

ACCTACGGCA AGGACCGCGA GTCCCGCTG TGGCTCGGCT CGCTGAAGTC GAACATCGGC 26580

CACGCGCAGG CCGCCGCGGG GGTCCCGGC GTCATCAAGA TGGTCCAGGC GTCCTCGCAC 26640

GAAGTCCTGC CGCCGACGCT GCACGTCGAC CGCCCTACCC CCGAGGTCGA CTGGTCGGCC 26700

GGTGCCGTCG AACTGCTGAC GGAAGCCCGC GAGTGGCCGC GCAACGGGCG CCCGCGCCGG 26760

GCCGGGGTCT CCGCGTTCGG CGTCAGCGGC ACGAACGCGC ACCTGATCCT GGAGGAGGCG 26820

CCCGCCCAAG AGCCGGTGCC CACACCCGAG GTTCCCTGG TGCCGGTCGT GGTCTCCGCG 26880

CGGAGCAGGG CGTCCCTGGC CCGTCAGGCC GGTGCGCTCG CCGGATTCGT GCGGGGTGAC 26940

GCGTCCTTGG CCGGTGTGEC CCGGGCGCTG GTGACGAACC GGGCCGCGCT GACCGAGCGC 27000

GCGGTCATGG TCGTGGGCTC TCGCGAAGAA GCCGTGACGA ACCTGGAAGC GCTGGCCCCG 27060

GGCGAAGACC CGGCCGCGGT GGTACCGGC CGGGCGGGTT CGCCGGGCAA GCTCGTCTGG 27120

GTCTTCCCCG GCCAGGGCTC GCAGTGGATC GGGATGGGCC GGGAACTCCT GGA CTCTTCG 27180

CCGGTCTTCG CCGAGCGGGT CGCCGAATGC GCGGCCGCC TGAACCGTG GATCGATTGG 27240

TACTGCTCG ACGTGCTCG CGGGGAGTCC GACCTGCTGG ACCGGGTCGA CGTCGTGCAG 27300

CCCGCCAGCT TCGCGATGAT GGTGGCCTG GCCGCGGTGT GGCAGTCGGT GGGTGTCCGC 27360

CCGGATGCCG TCGTCGGCCA CTCGCAGGGC GAGATCGCCG CCGCCTGCGT CTCGGGCGCG 27420

CTGTCGCTGC AGGACCCGC GAAGGTGGTT GCCTTGCGCA GCCAGGCGAT CGCCACCCGG 27480

CTGGCCGGGC GCGGCGGCAT GGCTTCCGTG GCGTTGAGCG AAGAAGACGC GACCGCGTGG 27540

CTGGCGCCGT GGGCCGACCG GTTCCAGGTG GCCGCGGTCA ACAGCCCTGC CTCCGTGGTG 27600

ATCGCCGGGG AAGCCAGGC CCTCGACGAG GTCGTCGACG CGTTGTCCGG TCAGGAAGTC 27660

CGCGTCCGGC GGGTGGCCGT GGA CTACGGG TCCCACACCA ACCAGGTCGA AGCCATCGAG 27720

GATCTGCTGG CCGAGACCTT GGCCGGCATC GAGGCGCAGG CCCCAGAGT GCCCTTCTAC 27780

TCGACCCTGA TCGGTGACTG GATCCGTGAC GCCGGGATCG TCGACGGCGG CTACTGGTAC 27840

CGGAACCTGC GCAACCAGGT CGGGTTCGGT CCGGCCGTG CGGAGCTCGT TCGCCAGGGC 27900

CACGGGGTGT TCGTCGAGGT CAGCGCGCAC CCGGTGCTGG TCCAGCCGCT CAGTGAATC 27960

AGCGACGACG CGGTGGTGAC CGGGTCGCTG CGGCGGAAG ACGGTGGCCT GCGCCGCCTG 28020

CTGACGTCGA TGGCCGAGCT GTACGTGCAG GGTGTCCCGC TCGACTGGAC CGCGGTCTG 28080

CCGCGGACCG GCCGGGTCGA CTGCCGAAG TACGCTTCG ACCACCGGCA CTACTGGCTG 28140

27060 27120 27180 27240 27300 27360 27420 27480 27540 27600 27660 27720 27780 27840 27900 27960 28020 28080 28140

CGGCCCCGCG AGTCCGCGAC CGACGCGGCT TCGCTGGGCC AGGCGGCGGC CGACCACCCG 28200

CTGCTGGGCG CGGTGCTCGA GCTGCCGCAG TCCGACGGCC TGGTGTTTAC CTCGCGGCTG 28260

TCCGTGCGGA CGCACCCGTG GCTGGCCGAC CACGCGGTG GTGGCGTGGT CATCCTCCCC 28320

GGCTCCGGGC TGGCCGAAC TGGCGTCCGG GCCGGCGACG AAGCCGGGTG CACCGCCCTC 28380

GACGAGCTGA TCATCGAAGC TCCGCTGGTC GTGCCGCCCC AAGGCGCGGT CCGCGTCCAG 28440

GTCGCGTTGA CGGCCCCGGA CGAGACCGGC TCGCGCACGG TGGACCTCTA CTCCCAGCGC 28500

GACGGCGGCG CGGGGACGTG GACGCGGCAC GCCACCGGCG TGCTGTGAC GGCCCCCGCT 28560

CAGGAACCCG AGTTCGACTT CCACGCCTGG CCGCCCGCGG ATGCCGAGCG GATCGACGTC 28620

GAGACCTTCT ACACCGACCT GGCCGAGCGT GGTACGGCT ACGGGCCGCG GTTCCAGGGG 28680

CTGCAAGCGG TGTGGCGGCG TGACGGCGAC GTCTTCGCCG AGGTGCGCCT GCCCGAGGAC 28740

CTGCGCAAGG ACGCGGGCCG GTTCGGCGTC CACCCGGCGC TGCTCGACGC GCGGCTGCAG 28800

GCCGCCACGG CCGTGGGCGG CGACGAGCCC GGTCAGCCGG TGCTGGCGTT CGCGTGGAAC 28860

GGCCTGGTCC TGCACGCCGC GGGCGCGTCG GCCCTGCGGG TCCGGCTCGC GCCGAGCGGC 28920

CCGGACACGC TGTCCGTGGC AGCCGCCGAC GAAACCGGCG GCTTGGTCCT GACCATGGAA 28980

TCGCTGGTCT CCCGGCCGGT TTCGGCCGAG CAGCTCGGCG CCGCGGCCGA CGCGGGCCAC 29040

GACGCGATGT TCCGCGTCGA CTGGACCGAG CTGCCTGCCG TGCCCCGCGC GGAAC TGCCG 29100

CCGTGGGTGC GGATCGACAC CGCCGACGAC GTCGCGGCCT TGGCGGAGAA GGCGGACGCA 29160

CCACCGGTGG TGGTCTGGGA AGCCGCCGGG GGAGACCCGG CCCTGGCCGT GAGTTCCCGG 29220

GTGCTCGAGA TCATGCAGGC CTGGCTGGCC GCGCCCGCGT TCGAGGAGGC CCGGCTGGTC 29280

GTGACGACCC GCGGCGCGGT ACCCGCCGGC GGTGACCACA CACTGACCGA CCCGGCCGCG 29340

GCCGCGGTGT GGGGCCTGGT CCGGTCCGCG CAGGCGGAAC ACCCGGACCG GGTCGTCTTG 29400

CTGGACACCG ACGGCGAAGT TCCGCTGGGC GCGGTGCTGG CCTCCGGTGA GCCGCAGCTC 29460

GCGGTGCGCG GAACGACGTT CTTCGTGCCC CGGCTGGCCC GCGCCACCCG GCTCTCGGAC 29520

GCGCCTCCTG CGTTCGACCC GGACGGGACC GTGCTGGTCT CGGGCGCCGG ATCGCTGGGC 29580

ACCTTGGTGG CCCGGCACCT GGTCACCCGG CACGGCGTGC GCCGGGTGGT GCTGGCCAGC 29640

CGGCAGGGCC GGGACGCCGA GGGCGCCCAG GACCTGATCA CCGAGCTCAC CGGCGAAGGC 29700

GCGGACGTGT CCTTCGTGGC CTGTGACGTC TCCGATCGCG ACCAGGTGGC CGCGCTGCTC 29760

GCGGGCCTCC CGGACCTGAC CGGGGTGGTG CACACCGCCG GCGTCTTCGA GGACGGCGTG 29820

ATCGAGGCGC TGACGCCCGA CCAGCTCGCG AACGTGTACG CGGCCAAGGT CACGGCCGCG 29880

ATGCACCTCG ACCAGCTCAC CCGCGACCGG GATCTCGGCG CGTTCGTCTG GTTCTCCTCC 29940

GTGCGGGGGG TGATGGGTGG TGGCGGTCAA GGCCCGTACG CGGCGGCGAA CGCCTTCCTG 30000

GACGCGGCEA TGGCGAGTCG TCAGGCCGCG GGCTGCCGG GCCTGTCCCT GCGGTGGGGC 30060

CTCTGGGAAC GCAGCAGCGG CATGGCCGCC CACCTCAGCG AGGTCGACCA CGCGCGGGCG 30120

AGCCGCAACG GTGTCCTGGA ACTGACCCGG GCCGAGGGCC TGGCGCTGTT CGACCTCGGG 30180

CTGCGGATGG CCGAGTCGCT GCTCGTGCCG ATCAAGCTCG ACCTCGCCGC GATGCGGGCG 30240

AGCACGGTCC CGGTCTGTGTT CCGCGGCCTG GTCCGGCCGA GCCGGACCCA GGCGCGCACG 30300

GCGTCCACTG TGGACCGGGG GCTGGCCGGG CGGCTCGCCG GGCTGCCGGT GGCCGAGCGG 30360

30360 30300 30240 30180 30120 30060 30000 29940 29880 29820 29760 29700 29640 29580 29520 29460 29400 29340 29280

GCGGCGGTGC TGGTCGACCT GGTGCGCGGG CAGGTCGCGG TCGTGCTCGG CTACGACGGG 30420

CCGGAGGCCG TCCGCCCGGA CACGGCGTTC AAGGACACCG GGTTCGACTC GCTGACGTCG 30480

GTGGAACTGC GCAACCGGCT GCGCGAGGCG ACCGGGCTCA AGCTCCCCGC CACGCTCGTC 30540

TTCGACTACC CGAACCCCTT GGCGGTGGCG CGCTACCTGG GCGCGCGGCT GGTCCCGGAC 30600

GGGACCGCGA ACGGCAACGG GAACGGGAAT GGGCACAGCG AAGACGACCG GCTGCGGCAC 30660

GCGCTGGCGG CCATCGCGGC CGAGGACGCG GCGGAGGAGC GGTGATCGC CGACCTGGGC 30720

GTCGACGACC TCGTGCAACT GGCTTTCGGC GACGAGTGAT TGGGGCAAGT GGTGAGTGCG 30780

TCGTATGAAA AGGTCGTCGA GGCGCTGCGG AAGTCGCTCG AAGAGGTCGG CACGCTGAAG 30840

AAGCGGAACC GGCAGCTCGC CGACGCGGCC GCGGAGCCGA TCGCCATCGT CGGCATGGCC 30900

TGCCGGCTGC CCGGTGGCGT CACCGGGCCC GGTGACCTCT GCGGGCTGGT GGCCGAGGGC 30960

GGCGACGCCG TCTCGGGGTT CCCCACCGAC CGCTGCTGGG ACCTGGACAC CCTGTTCGAC 31020

CCGGATCCCG ACCACGCGGG GACGTCGTAC ACCGACCAGG GCGGCTTCCT CCACGACGCG 31080

GCCCTGTTCG ACCCGGGCTT CTTCGGGATT TCGCCGCGCG AGGCGCTGGC CATGGACCCG 31140

CAGCAGCGGT TGCTGCTGGA GCGTCCTGG GAGGCGCTGG AAGGTGTCGG CCTCGACCCG 31200

GCTTCGTTGC AGGGCACCGA CGTCGGCGTG TTCACCGGCG CGGGCGGGTC GGGCTACGGC 31260

GGCGGCCTCA CCGGGCCGGA GATGCAGAGT TTCGCGGGCA CCGGGCTGGC CTCGAGCGTG 31320

GCTTCGGGCC GGGTGTCTTA CGTCTTCGGG TTCGAGGGAC CGGCGGTAC GATCGACACG 31380

GCGTGCTCGT CGTCGCTGGT GCGGATGCAC CTCGCCGCGC AGGCCCTGCG CCAAGGCGAC 31440

TGCTCGATGG CACTGGCCGG CGGCGCGATG GTGATGTCGG GCCCCGACTC CTTCGTCGTC 31500

TTCTCCCGGC AGCGGGGGCT GGCCACCGAC GGGCGGTGCA AGGCGTTCGC GTCGGGCGCC 31560

GACGCCATGG TGCTCGCCGA GGGCATCAGC GTGGTCGTGC TGGAGCGGCT TTCGGTCGCG 31620

CGGGAACGCG GGCACCGGGT GCTGGCCGTG CTGCGCGGCA GCGCGGTGAA CCAGGATGGC 31680

GCGTCEAACG GCCTGACCGC CCCGAACGGC CCTTCCCAGC AGCGCGTGAT CCGCGCCGCG 31740

CTEGCCAACG CCGGAATCGG ACCGTCCGAT GTGGACCTCG TCGAGGCGCA CGGGACCGGG 31800

ACGAGCCTGG GTGATCCCAT CGAGGCGCAG GCCTTGCTGG CGACCTACGG CCAGGACCGG 31860

GAGACGCCGT TGTGGCTCGG CTCGCTGAAG TCGAACATCG GGCACACGCA GGCGGCCGCG 31920

GGCGTGCCGA GCGTGATCAA GGTCTGTGAG GCGCTGCGGC ACGGCGTCAT GCCGCCGACC 31980

CTGCACGTGC ACGAGCCCAG CTCGCAGGTC GACTGGTCCG AAGGCGCGGT GGAAGTGTG 32040

ACCGGGAGCC GGGACTGGCC GCGCGGGGAC CGGCCGCGCC GGGCCGGGGT GTCGTGTTTC 32100

GGCGTCAGCG GGACGAACGT GCACCTGATC ATCGAGGAAG CCCCCGAGGA GCCCGCTGCG 32160

GCCGTGCCGA CGTCCGCGGA CGTCGTGCCG CTGGTGGTTT CCGCACGCAG CACGGGTTC 32220

CTGGCCGGTC AGGCCGACCG GCTGACCGAG GTGGACGTCC CCCTCGGACA CCTCGCCGGG 32280

GCGCTGGTGG CCGGGCGCGC GGTGCTCGAG GAACGCGCGG TCGTGGTCGC CGGTTCGGCC 32340

GAAGAAGCCC GCGCGGGGCT GGGTGCGCTG GCTCGCGGTG AAGCCGCGCC CGGCGTCGTG 32400

ACCGGGACCG CGGGCAAGCC GGGCAAGGTC GTCTGGGTGT TCCCGGACA GGGGACGCAG 32460

TGGGTGGGCA TGGGCCGGGA GCTCCTCGAC GCGTCCCCGG TGTTGCCGA GCGGATCAAG 32520

GAGTGCGCGG CGGCACTGGA CCAGTGGACC GACTGGTCGC TGCTGGACGT CCTGCGTGGT 32580

CGCTGCTGCT

GACGGTGACC TGGATTCTGT CGAGGTGCTG CAGCCCGCGT GCTTCGCGGT GATGGTGGGG 32640

CTGGCCGCGG TCTGGGAGTC GGC GGCGGGGTC CGGCCGACG CCGTCGTCGG CCACTCGCAG 32700

GGCGAGATCG CCGCGGCCTG CGTGTCCGGC GCGCTCACC TCGACGACGC CGCGAAGGTG 32760

GTGGCCCTGC GCAGCCAGGC GATCGCGGCG CGGCTGTCCG GCCGCGGCGG GATGGCGTCG 32820

GTCGCGTTGA GCGAGGACGA GGCGAACGA CGGCTGGGTT TGTGGGACGG CCGGATCGAG 32880

GTGGCCGCGG TCAACGGCCC CGCCTCCGTG GTGATCGCGG GGGACGCCCA AGCCCTCGAC 32940

GAGGCTTTGG AGGTGCTGGC CGGGGACGGC GTCCGCGTCC GGCAGGTCGC GGTCGACTAC 33000

GCCTCCCACA CCCGGCACGT CGAGGACATC CGCGACACC TCGCCGAGAC GCTGGCCGGG 33060

ATCACCGCGC AGGCCCCGGA CGTGCCGTTT CGCTCCACCG TCACCGGCGG CTGGGTGCGG 33120

GACGCCGACG TCCTGGACGG CGGGTACTGG TACCGCAACC TGCGCAACCA GGTCCGGTTC 33180

GGCCCGGCCG TGGCCGAGCT GCTCGAGCAG GGCCACGGGG TGTTCTGTCG GGTCAGCGCC 33240

CACCCCGTGC TGGTGCAGCC GATCAGCGAG CTCACCGACG CCGTCGTCAC CGGGACGCTG 33300

CGGCGCGACG ACGGCGGCCT GCGCCGCCTG CTGACGTCGA TGGCCGAGCT GTTCGTCCGC 33360

GGTGTTTCGG TCGACTGGGC CACGCTGGTG CCGCCCGCGC GCGTGGACCT CCCGACGTAC 33420

GCCTTCGACC ACCAGCACTT CTGGCTCCGG CCGGCCCGCG AGGCGGACGC CGTCTCGCTC 33480

GGCCAGGCCG CGGCGGAGCA CCCGCTGCTC GGCGCGGTG TCCGGCTGCC GCAGTCGGAC 33540

GGCCTGGTCT TCACCTCGCG GCTGTGCTG CGGACGCACC CGTGGCTGGC CGACCACACC 33600

ATCGGCGGCG TGGTGCTGTT CCCCAGCACC GGGCTGGTCG AACTGGCCGT GCGGGCCGGC 33660

GACGAGGCCG GGTGCCCCGT CCTGGACGAA CTCGTGACCG AGGCGCCGCT GGTCTGTCCC 33720

GGGCAGGGCG GAGTGAACGT CCAGGTCACG GTGAGCGGCC CGGACCAGAA CGGCTTGCGC 33780

ACGGTGGACA TCCACTCCCA GCGCGACGAC GTGTGGACCC GGCACGCGAC CGGAACGGTC 33840

TCGGCGACCC CGGCGAGCAG CCCC GGCTTC GACTTCACCG CGTGGCCGCC GCCGGACGGG 33900

CAGCGCGTCG AGATCGGCGA CTTCTACGCC GACCTCGCCG AGCGCGGGTA CGCGTACGGG 33960

CCCTTGTTCC AGGGCGTGCG GCGGGTGTGG CAGCGCGGCG AAGACGTGTT CGCCGAGGTC 34020

GCGCTGCCCCG AAGACCGGCG GGAGGACGCC GCCCGGTTTC GCTTGACCCC GCGGTTGCTG 34080

GACGCGGCCC TGCAGACCGG GACGATCGCC GCGGCCGCGT CCGGTCAGCC GGGCAAGTCC 34140

GTEATGCCGT TCTCGTGGA CCGGCTGGCG CTGCACGCCG TCGGGGCCGC GGGCTCCGG 34200

GTCCGCGTGG CCCCCGGCG ACCGGACGCG CTGACCGTCG AGGCCGCCGA CGAGACCGGC 34260

GCCCCGGTCC TCACCATGGA CTCGCTGATC CTGCGTGAAG TCGCCCTCGA CCAGCTGGAC 34320

ACTGCGCGCG CCGGCTCGCT CTACCGGGTG GACTGGACGC CACTGCCAC TGTGGACAGT 34380

GCGGTGCCCCG CTGGTCGGGC CGAGGTGCTG GAAGCTTTTC GCGAGGAGCC CCTGGACCTG 34440

ACCGGCCGGG TGCTGGCCGC CCTGCAGGCG TGGCTTTCCG ACGCGGCGGA GGAAGCCCGC 34500

CTGGTCGTGG TGACCCGGGG TCGGTTGCC GCCGGAGACG GTGTGGTGAG CGATCCGGCG 34560

GGTGCCGCGG TGTGGGGCCT GGTCCGGGCC GCGCAGGCGG AGAACCCGGA CCGGTTCTGTC 34620

CTGCTCGACA CCGACGGCGA GGTGCCGCTG GAAGCGGTGC TGGCGACCGG TGAGCCGCAG 34680

CTCGCGCTGC GCGGCACGAC GTTCTCGGTG CCCC GGCTCG CCCGCGTCAC CGAACCGGCG 34740

GAAGCCCCGC TGACGTTCCG TCCGGACGGG ACGTCTCTGG TCTCCGGCGC CGGGACGCTG 34800

GGTGCCTCG CCGCCGCGA CCTCGTCACC CGGCACGGCG TCCGGCGGCT CGTGCTGGCC 34860

AGCCGGCGCG GCCGGGCGC CGAGGGCATC GACGACCTCG TCGCCGAGCT GACCGGGCAC 34920

GGCGCCGAAG TGACGGTCGC CGCCTGCGAC GTCTCCGACC GCGACCAGGT GCGGGCGCTG 34980

CTCAAGGAAC ACGCGCTGAC CGCGGTGGTG CACACGGCGG GCGTGTTTCA CGCCGGTGTC 35040

ACCGGCGCGC TGACCCGGGA GCGGCTGGCC AAGGTGTTTCG CGCCAAGGT CGACGCGGCC 35100

AACCACCTCG ACGAGCTGAC CCGCGACCTG GACCTCGACG CGTTCATCGT CTACTCGTCC 35160

GCCTCCTCGA TCTTCATGGG CGCGGGCAGC GCGGGGTACG CGGCGGCGAA CGCCTACCTC 35220

GACGGCCTGA TGGCCGCCCCG GCGCGCGGCG GGCCTGCCGG GGCTGTTCGT GGCTTGGGGC 35280

CCGTGGGAGC AGCTCACC GG CATGGCCGAC ACCATCGACG ACCTCACCCT GGCCCGGATG 35340

AGCCGGCGCG AAGGCCGCGG CGGCGTCCGC GCGCTCGGCT CCGCCGACGG CATGGAGCTG 35400

TTCGACGCCG CGCTCGCGGC CGGGCAGGCG CTGCTGGTGC CGATCGAGCT CGACCTGCGC 35460

GAGGTGCGGG CCGACGCGGC CGGCGGCGGC ACGETGCCGC ACCTGCTGCG CGGGCTGGTC 35520

CGCGCGGGCC GGCAGGCGGC GCGGACGGCG GCCACCGAGG ACGGCGGCCT GGAACGCCGG 35580

CTGGCCGGGC TCACCGTGGC CGAACAGGAA GCGCTGCTGC TCGACCTCGT CCGCGGTCAG 35640

GTCGCCGTCG TGCTCGGGCA CGCCGACAGC TCCGGCGTCC GCGCCGACGC GCGGTTCAAG 35700

GACGCCGGGT TCGACTCGCT GACGTGGTG GAGCTGCGCA ACCGGCTGCG CGAGACGACC 35760

GGCCTGAAAC TGCCCGCGAC GCTGGTCTTC GACCATCCGA ACCCGCTGGC ACTGGCCCCG 35820

CACCTCGGG CGGAACTCGC CGTCGACGAG GCATCCCCGG CCGATGCGGT GCTGGCCGGG 35880

CTCGCCGGGC TGGAGGCGGC CATCGCGGCC GCCGGCGCCC CGGACGGCGA CCGGATCACC 35940

GCGCGGCTGC GGGAACTGCT CAAGGCCGCC GAGGCGGCCG AGGCCCCGCC GGGCACCTCC 36000

GGCGATCTCG ACACGGCCAG CGACGAGGAA CTGTTGCCCC TCGTCGACGG GCTCGACTGA 36060

AACCGCTGTG ACATCCGGGG CTTCGCCACC CGGGCCCCGA AAAGCAAGCA CACGTGAGAG 36120

TTCTGGGAGT TGAGTTCAGT GGCTGACGAG GGACAACTCC GCGACTACCT CAAGCGGGCC 36180

ATCGCCGACG CCCGCGACGC CCGCACGCGG CTGCGCGAGG TCGAGGAGCA GCGCGGGAG 36240

CCGATCGCCA TCGTCGCCAT GGCGTGCCGG TACCCGGGCG GGGTGTCTC GCCCGAGGAC 36300

CTGTGGCGGC TGGTGGCCGA GGGGACCGAC GCCGTCTCCG CGTTCCCCGG CGACCGCGGC 36360

TGGGACGTCG ACGGGCTCGT CGACCCGGAC CCCGACCGCC CGGGCACGAC GTACACGGAC 36420

CAGGGTGGCT TCCTCCACGA GGCCGGCCTC TTCGACGCGG GGTTCCTTCG GATCTCGCCG 36480

CGGGAGGCCG TCGCGATGGA CCCGCAGCAG CGGCTGCTGC TGGAGACGTC CTGGGAGGCC 36540

ATCGAACGCA CCGGCACCGA CCCGCTTTCG CTGAAGGGCA GCGACATCGG CGTCTTCACC 36600

GGCGTCGCGA GCATGGGTTA CGGCGCCGGT GCGGCGTGG TCGCGCCGA GCTGGAGGGT 36660

TTCGTGCGCA CCGGTGCGGC GCCGTGCATC GCGTCCGCC GGGTGTGTA CGTCCTCGGC 36720

TTCGAAGGCC CGGCGTAC CGTCGACACC GGGTGTTCGT CGTCGCTGGT GGCGATGCAC 36780

CTCGCCGCGC AGGCGCTGCG GCGGGGTGAG TGCTCGATGG CTCTGGCCGG CGGCGCGATG 36840

GTGATGGCCC AGCCGGGTTC GTTCGTGTCC TTCTCGCGC AACCGGGCT CGCCCTGGAC 36900

GGGCGCTGCA AGGCGTTTTT GGACAGCGCC GACGGGATGG GACTGGCCGA GGGCGTCGGC 36960

GTCATCGCGC TGGAACGGCT GTCGGTCGCC CGTGAGCGTG GGCACCGGGT GCTGGCCGTG 37020

20250304 15:00:00

CTGCGCGGTA TCGCGGTGAA CCAGGATGGC GCGTCGAACG GCTTGACCGC CCCGAACGGC 37080

CCGTCCCAGC AGCGGGTGAT CCGCGCCGCG CTGGCCGAAG CCGGGCTGTC GCCGTCCGAT 37140

GTGGACGCCG TCGAAGGGCA CGGGACGGGC ACGACGCTGG GCGATCCGAT CGAAGCGCAG 37200

GCGTTGCTGG CCACCTACGG CAAGGGCCGG GACCCGGAGA AGCCGCTCTG GCTGGGCTCG 37260

GTGAAGTCGA ACCTCGGGCA CACGCAAGCG GCCGCGGGCG TGGCCAGCGT GATCAAGATG 37320

GTGCAGGCGC TCGGCCACGG CGTGCTGCCC CCGACGCTGC ACGTCGACCG GCCGTCCACC 37380

GAAGTCGACT GGTGCGCCGG TCGGTCTCG CTGTTGACGG AGGCTCGGGA GTGGCCGCGC 37440

GAAGGGCGGC CGCGCCGGC CGGGGTGTCC TCGTTCGGGA TCAGCGGGAC CAACCGGCAC 37500

CTCATCCTGG AGGAAGCGCC CGAGGAGGAG CCGCCCGTCG CCGAAGCGCC TTCCGCCGGA 37560

GTGGTGCCCC TGGTGGTGTC GGCTCGTGGG GCCCTGGCGG GTCAGGCCGG CCGGCTGGCC 37620

GCGTTCCTCG AGGCGTCCGA CGAGCCGTTG GTGACCGTCG CCGGGGCGCT GATCTGCGGC 37680

CGGTCCCAGT TCGGCGACCG GGCCGTCGTG GTGGCGGGCA CGCGCGCAGA GGCGACGGCC 37740

GGGCTGGCCG CGCTGGCCCC CGGCGAAAGC GCCGCCGACG TCGTGACCGG CACGGTCGCG 37800

GCCTCGGGCG TGCCGGGCAA GCTCGTGTGG GTGTTCCCGG GCCAGGGTTC GCAGTGGGTG 37860

GGCATGGGCC GGGAGCTCCT CGAAGCCTCG CCGGTGTTG CCGCGCGGAT CGCGGAGTGC 37920

GCGGCTGCCC TCGAACCGTG GATCGACTGG TCGCTGCTGG ACGTCCCTCCG TGGCGAGGGC 37980

GACCTCGACC GCGTCGACGT GGTGCAGCCC GCGAGTTTCG CCGTGATGGT CGGCCTGGCC 38040

GCGGTGTGGT CGTCCGTCGG GGTGGTGCCC GACGCGGTGC TCGGGCACTC GCAGGGGGAG 38100

ATCGCGGCGG CGTGCGTGTC GGGGGCGTTG TCGCTGCAGG ACGCGGCGAA GGTGGTCGCG 38160

TTGCGCAGCC AGGCGATCGC GGCGAAGCTG GCCGGCCGCG GCGGCATGGC CTCGGTCGCG 38220

CTGAGCGAGG AAGACGCGGT CGCGCGGTTG CGGCACTGGG CGGACCGGGT CGAGGTGGCC 38280

GCGGTCAACA GCCCGTCGTC GGTGGTGATC GCCGGCGACG CCGAAGCCCT CGACCAGGCC 38340

CTCGAAGCAC TGACCGGCCA GGACATCCGG GTCCGGCGGG TGGCGGTGGA CTACGCCTCG 38400

CACACCCGGC ACGTCGAAGA CATCCAGGAG CCCCTCGCCG AGGCACTGGC CGGGATCGAG 38460

GCGCACGCGC CGACCCTGCC GTTCTTCTCG ACCCTCACCG GTGACTGGAT TCGCGAAGCG 38520

GGCGTCGTGG ACGGCGGCTA CTGGTACCGG AACCTGCGCA ACCAGGTCGG TTTCGGCCCG 38580

GCGGTGGCCG AGCTGCTCGG CCTCGGCCAC CGGGTGTTCTG TCGAGGTCAG CGCGCACCCC 38640

GTGCTCGTCC AGGCGATCAG CGCGATTGCC GACGACACCG ACGCGGTCGT CACCGGCTCG 38700

CTGCGGCGCG AGGAGGGCGG CCTGCGGCGG CTGCTGACGT CGATGGCCGA GCTGTTCGTC 38760

CGCGGAGTCG ACGTGGA CTG GGCCACGATG GTGCCGCCAG CGCGGGTCGA TTTGCCGACC 38820

TACGCCTTCG ACCACCAGCA CTACTGGCTG CGGTACGTCG AGACCGCGAC CGACCGGGCC 38880

GGTCCGGTGG TCCGGCTGCC GCAGACGGGC GGCCTGGTCT TCACCACCGA GTGGTCGCTG 38940

AAGTCACAGC CGTGGCTGGC CGAGCACACC CTGGAAGACC TGGTCGTCGT CCCC GGCGCG 39000

GCACTGGTCG AGCTGGCCGT CCGGGCCGGT GACGAGGCCG GGACCCCGGT GCTGGACGAA 39060

CTCGTCATCG AGACGCCCT GGTCTGTCG GAACGCGGCG CGATCCGGGT GCAGGTCACG 39120

GTGAGCGGAC CGGACGACGG CACACGGACC CTGGAAGTGC ATTCCCAGCC CGAAGACGCC 39180

ACCGACGAAT GGACCCGGCA CGCCACCGGC ACGCTGTCGG CGACCCCGGA CGAAGCAGC 39240

2025032409

GGGTTGACT TCACGGCCTG GCCGCCCCCG GGCGCCCGGC AGCTCGACGG CGTTCCGGCG 39300

ATCTGGCGGG CCGGCGACGA GATCTTCGCC GAAGTCTCCC TGCCCCGACGA TGCGGACGCC 39360

GAGGCATTCG GCATCCACCC CGCGCTCCTG GACGCGGCC TGCACCCCGC CCTGCCCCGGC 39420

GATGACGGTC TGACGCAGCC CATGGAATGG CGTGGCCTGA CGCTGCACGC CGCGGGGGCG 39480

TCGACGCTGC GGGTCCGGTT GGTGCCCGGC GGGTTCCTGG AAGCGCCGA CGGCGCCGGC 39540

AGCCTGGTCG TCACGGCGAA GGAGGTTGCC CTCCGCCCGG TGACGATCGC GCGGTCGCGC 39600

ACCACCACCC GAGACTCGCT GTTCCAGCTG AACTGGATCG AGCTGCCCCGA GAGTGGCGTG 39660

GTGGCCGCGG CAGACGACAC CGAGGTGCTG GAGGTGCCCG CGGGCGATTC CCCGCTGGCG 39720

GCGACCTCCC GAGTCTTGGA GCGGCTCCAG ACCTGGCTGA CCGAGCCCGA GCGGGAACAG 39780

CTGGTCGTCG TGACGCGCGG CGCGGTGCCC GCCGGGGACA CCCCAGTGAC CGACCCGGCC 39840

GCGGCGGCGG TCTGGGGCCT GGTCCGGTCC GCGCAGGCGG AGAACCCGA CCGGATCGTC 39900

CTGCTCGACA CCGACGGCGA AGTCCCGCTG GGTGCGGTGC TGGCCGGCGG CGAGCCGCAG 39960

GTCGCGGTGC GCGGCACGGC GCTGTACGTC CCGCGCCTGG CCCGCGCCGA CGCGGCCCCG 40020

GTATCCGGTC TACATGGGAC GGTCTCTGTC TCCGGTGCCG GTGTGCTCGG CGAGATCGTG 40080

GCGCGGCACC TGGTCACCCG CCACGGCGTG CGCAAGCTGG TGCTCGCCAG CCGCCGCGGC 40140

CTGGACGCCG ACGGCGCGAA GGACCTCGTC ACCGACCTCA CCGGCGAGGG CGCGGACGTG 40200

TCCGTCTGTCG CCTGCGACCT GGCCGATCGG AACCAGGTGG CCGCGCTGCT GGCCGACCAC 40260

CGCCCGGCGA GCGTCATCCA CACGGCGGGC GTCTCGACG ACGGCGTCAT CGGGACGCTG 40320

ACCCCGGAGC	GGCTGGCCAA	GGTGTTCGCG	CCCAAGGTCG	ACGCGGTCCG	CCATCTCGAC	40380
GAGCTGACTC	GCGACCTCGA	CCTCGACGCG	TTCGTCTGT	TCTCCTCCGG	CTCCGGCGTG	40440
TTCGGTTCGC	CGGGGCAGGG	CAACTACGCG	GCGGCGAACG	CGTTCCTGGA	CGCGGCGATG	40500
GCGAGCCGCC	GCGCGGCGGG	TCTTCCTGGT	CTCTCGCTGG	CGTGGGGCCT	GTGGGAACAG	40560
GCCACCGGCA	TGACCGCGCA	CCTCGGCGGC	ACCGACCAGG	CCCGGATGAG	CCGGGGCGGG	40620
GTGCGGCCGA	TCACGCGCGA	GGAAGGCATG	GCCCTGTTCG	ACACGGCACT	GGGTGCGCAG	40680
CCCGCGCTGC	TCGTGCCGGT	CAAGCTCGAC	CTGCGGGAGG	TGCGGGCCGG	CGGGGCCGTG	40740
CCGCACCTGC	TGCGCGGGCT	GGTCCGGGCC	GGCGGGCGGC	AGGCCCAAGC	CGCGTCCACA	40800
GTGGACAACC	AGCTGCTGGG	CCGGCTGGCC	GGGCTGGGCG	CGCCCGAGCA	GGAGGCGCTG	40860
CTCGTCGACC	TCGTGCGCGG	CCAGGTCGCG	GCGGTGCTCG	GGCACGCCGG	GCCGGACGCG	40920
GTCCGCGCCG	ACACGGCGTT	CAAGGACGCC	GGGTTCGACT	CGCTCACCTC	GGTCGACCTG	40980
CGCAACCGGC	TGCGGGAGAG	CACCGGGCTG	AAGCTGCCCC	CCACGCTCGC	CTTCGACTAC	41040
CCGACCCCGC	TGGTCTCTGC	CCGGCACCTG	CGTGACGAGC	TCGGGGCCGG	CGACGACGCG	41100
CTTTCGGTGG	TGCACGCGCG	GCTCGAAGAC	GTCGAGGCGC	TGCTCGGCGG	GCTGCGCCTC	41160
GACGAATCCA	CGAAGACCGG	TCTCACCTC	CGGCTGCAGG	GCCTGGTCGC	CCGGTGCAAC	41220
GGCGTGAACG	PCCAGACCGG	CGGCGAAACG	CTGGCGGACC	GGCTCGAGGC	CGCGTCCGCC	41280
GACGAAGTCC	TCGACTTCAT	CGACGAGGAG	CTEGGTCTCA	CCTGACCCCG	GTTCGAGACC	41340
GACGTTCCAG	CAACCCTTGT	GAGGACCCGA	GAATGGCCAC	GGACGAGAAA	CTCCTCAAAT	41400
ACCTCAAGCG	CGTCACGGCG	GAGCTGCACA	GCCTGCGCAA	GCAGGGTGCC	CGGCACGCCG	41460

ACGAGCCGCT CGCCGTCGTC GGGATGGCCT GCCGGTTCCC GGGTGGGGTG TCCTCGCCCC 41520

AAGACCTGTG GCAGCTCGTG GCCGGCGGGG TCGACGCCCT TTCGGAATTC CCCGACGACC 41580

GGGGCTGGGA GCTGGACGGC CTGTTTCGACC CGGACCCCGA CCACCCCGG ACGTCGTACA 41640

CCAGCCAGGG CGGCTTCCTG CGTGGCGCCG GGCTGTTTGA CGCGGGCCTG TTCGGCATCT 41700

CGCCGCGCGA GGCCCTCGTC ATGGACCCGC AGCAGCGGGT GCTGCTGGAG ACGTCGTGGG 41760

AGGCCCTCGA AGACGCCGGG GTCGACCCGC TTTCGCTGAA GGGCAGCGAC GTCGGCGTGT 41820

TCTCCGGCGT CTTACCCAG GGCTACGGCG CCGGGGCGAT CACGCCGGAC CTCGAGGCGT 41880

TCGCGGGCAT CGGGGCGGGG TCGAGCGTGG CGTCGGGCCG GGTGTCCTAC GTCTTCGGGC 41940

TGAAGGACC GGCGGTCACC ATCGACACCG CGTGTTCGTC GTCGCTGGTG GCCATCCACC 42000

TCGCCGCGCA GGCCCTGCGC GCGGGCGAGT GCTCGATGGC GCTCGCCGGC GGGGCGACGG 42060

TGATGCCGAC GCCCAGCACC TTCGTGCGGT TCTCGCGGCA GCGGGTGCTG GCTGCCGACG 42120

GCCGGTCCAA GGCCTTCTCC TCGACCGCGG ACGGCACCGG CTGGGCCGAG GGCGCCGGGG 42180

TGCTCGTCCT CGAACGGCTT TCGGTCGCGC AGGAGCGCGG CCACCGGATT CTCGCCGTGC 42240

TGCGCGGCAG CGCGGTCAAC CAGGATGGCG CCTCCAACGG CCTGACCGCG CCGAACGGGC 42300

CTTCGCAGCA GCGGGTGATC CGCAAGGCGC TCGCGGGCGC CGGGCTGGTC GCGTCCGATG 42360

TGACGTCGT GGAGGCGCAC GGCACGGGCA CCGCGCTGGG CGACCCGATC GAAGCGCAGG 42420

CGCTGCTGGC GACCTACGGC CAGGGCCGTG AGCGGCCGCT GTGGCTGGGG TCGGTCAAGT 42480

CGAACTTCGG GCACACGCAG GCGGCCGCCG GGGTCGCGGG CGTGATCAAG ATGGTCCAGG 42540

CCCTGCGGCA CGGCGCCATG CCGCCGACCC TGCACGTGGC CGAGCCGACG CCGGAGGTTCG 42600

ACTGGTCGGC CCGTGCGGTG GAACTGCTGA CCGAGCCGCG CGAGTGCCCC GCCGGTGATC 42660

GGCCGCGCCG GGCCGGGGTG TCCGCGTTTCG GGATCAGCGG GACGAACGCC CACCTGATCC 42720

TGAGGAGGC GCCCCCGGCC GACGCGGTTCG CGGAAGAACC GGAGTTCAAG GGGCCGGTGC 42780

CGCTGGTCGT CTCGGCGGGC AGCCCCACAT CTTTGCCGGC TCAGGCCGGC CGGCTCGCGG 42840

AGGTCTTGGC GTCCGGTGGT GTGTCCCGGG CCCGGCTGGC GAGCGGGCTG CTGTCGGGCC 42900

GGGCGCTGCT CCGTGACCGC GCGGTCTGTG TCGCGGGAAC GGACGAGGAC GCGGTGGCCG 42960

GGTTGCGTGC GCTGGCCCCG GGGGACCGCG CGCCCGGCGT GCTGACCGGT TCGGCCAAGC 43020

ACGGCAAGGT CGTCTACGTC TTCCCCGGCC AGGGTTCGCA GCGGCTCGGG ATGGGCCGCG 43080

AGCTCTACGA CCGGTACCCG GTGTTTCGGA CGGCGTTCGA CGAGGCTTGC GAGCAGCTGG 43140

ACGTCTGTCT GGCCGGCCGT GCCGGGCACC GCGTGCGGGA CGTCGTGCTC GGCGAAGTGC 43200

CCGCCGAAAC CGGGCTGCTG AACCAGACGG TCTTCACCCA AGCCGGGCTG TTCGCGGTGG 43260

AGAGCGCGCT GTTCCGGCTC GCCGAATCCT GGGGTGTCCG GCCGGACGTG GTGCTCGGCC 43320

ACTCCATCGG GGAGATCACC GCCGCGTATG CCGCGGGCGT CTTCTCGCTG CCGGACGCCG 43380

CCCGGATCGT CGCGGCGCGC GGCCGGCTGA TGCAGGCGCT GGCGCCGGGC GGGGCGATGG 43440

TCGCCGTGCG CGCCTCCGAA GCCGAGGTGG CCGAACTGCT CGGCGACGGC GTGGAAGTCG 43500

CCGCCGTCAA CGGCCCTTCG GCGGTAGTCC TTTCCGGGGA CGCGGACGCG GTCGTCGCGG 43560

CCGCCGCCCG CATGCGCGAG CGCGGGCACA AGACCAAGCA GCTCAAGGTT TCGCACGCGT 43620

TCCACTCCGC GCGGATGGCG CCGATGCTGG CGGAGTTCGC CGCCGAGCTG GCCGGCGTGA 43680

CGTGGCGCGA GCCGGAGATC CCGGTGGTCT CCAACGTGAC CGGCCGGTTC GCCGAGCCCC 43740

GCGAACTGAC CGAGCCGGGC TACTGGGCCG AGCACGTGCG GCGGCCGGTG CGGTTGCGCCG 43800

AGGGCGTCGC GGCCGCGACG GAGTCCGGCG GCTCGCTGTT CGTGGAGCTC GGGCCGGGGG 43860

CGGCGCTGAC CCCCCTCGTC GAGGAGACGG CCGAGGTCAC CTGCGTCGCG GCCCTGCGGG 43920

ACGACCGCCC GGAGGTCACC GCGCTGATCA CCGCGGTCGC CGAGCTGTTC GTCCGCGGGG 43980

TTGCGGTGCA TTGGCCGGCC CTGCTGCCGC CGGTCACCGG GTTCGTCGAC CTGCCGAAGT 44040

ACGCCTTCGA CCAGCAGCAC TATTGGCTGC AGCCCGCCGC GCAGGCCACG GACGCGGCCT 44100

CGCTCGGGCA GGTGCGGGCC GACCACCCGC TGCTGGGCGC GGTGGTCCGG CTGCCGCAGT 44160

CGGACGGCCT GGTCTTCACC TCGCGGCTGT CATTGAAATC GCACCCGTGG CTGGCCGACC 44220

ACGTCATCGG CGGGGTGGTG CTCGTCGCGG GCACCGGGCT CGTCGAGCTG GCCGTCCGGG 44280

CCGGGGACGA GGCCGGCTGC CCGGTCCTCG AAGAACTCGT CATCGAGGCT CCGCTGGTCG 44340

TCCCCGACCA CGGCGGGGTC CGGATCCAGG TCGTCGTGGG GGCACCGGGG GAGACCGGTT 44400

CGCGCGCGGT CGAGGTGTAC TCCCTGCGCG AGGACGCCGG TGCCGAAGTG TGGGCCCCGC 44460

ACGCCACCGG GTTCCTGGCT GCGACGCCGT CGCAGCACAA GCCGTTGAC TTCACCGCCT 44520

GGCCGCCGCC CGGCGTCGAG CGCGTCGACG TCGAGGACTT CTACGACGGC CTCGTCGACC 44580

GCGGGTACGC CTACGGGGCC TCGTTCCGGG GCCTGCGGGC GGTGTGGCGG CGCGGCGACG 44640

AAGTGTTCGC CGAGGTCGCC CTGGCCGAGG ACGACCGCGC GGACGCGGCC CGGTTGCGCA 44700

TCCACCCCGG CCTGCTGGAC GCCGCCCTGC ACGCGGGCAT GGCCGGTGCC ACCACCACGG 44760

AAGAGCCCCG CCGGCCGGTG CTGCCGTTCTG CCTGGAACGG CCTGGTGCTG CACGCGGCCG 44820

GGGCGTCCGC GCTGCGGGTC CGGCTCGCCC CGAGCGGTCC GGACGCCCTG TCGGTCGAGG 44880

CCGCGGACGA GGCCGGCGGT CTCGTTGTGA CGGCGGACTC GCTGGTCTCC CGGCCGGTGT 44940

CGGCCGAACA GCTGGGCGCG GCGGCGAACC ACGACGCGTT GTTCCGCGTG GAGTGGACCG 45000

AGATTTCCTC GGCTGGAGAC GTTCCGGCGG ACCACGTCGA AGTGCTCGAA GCCGTCGGCG 45060

AGGATCCCCCT GGAAC TGACC GGCCGGGTCC TGGAGGCCGT GCAGACCTGG CTCGCCGACG 45120

CAGCCGACGA CGCTCGCCTG GTCGTGGTGA CCCGCGGCGC CGTCCACGAG GTGACTGACC 45180

CGGCCGGTGC CGCGGTGTGG GGCCTGATCC GGGCCGCGCA GGCGGAAAAC CCGGACCGGA 45240

TCGTGCTGCT GGACACCGAC GGTGAAGTGC CGCTAGCCCG GGTGCTGGCC ACCGGCGAGC 45300

CCCAAACAGC CGTCCGAGGC GCCACGCTGT TCGCCCCGCG GCTGCCCCGC GCCGAGGCCG 45360

CGGAGGCACC GGCAGTGACC GGCGGGACGG TCCTGATCTC GGGCGCCGGC TCGCTGGGCG 45420

CGCTCACC GC CCGGCACCTG GTCGCCCCGC ACGGAGTCCG GCGGCTGGTG CTCGTCAGCC 45480

GCCGTGGCCC CGACGCCGAC GGCATGGCCG AACTGACCGC TGAAC TCATC GCTCAGGGCG 45540

CCGAGGTCCG CGTAGTCGCT TGCGACCTGG CCCACCGGGA CCAGGTCCCG GTACTGCTGG 45600

CCGAGCACCG CCCGAACGCC GTCGTGCACA CGGCCGGTGT TCTCGACGAC GGCGTCTTCG 45660

AGTCGCTGAC GCGGGAGCGG CTGGCCAAGG TCTTCGCGCC CAAAGTTACT GCTGCCAATC 45720

ACCTCGACGA GCTGACCCGC GAACTGGATC TTCGCGCGTT CGTCGTGTTT TCCTCCGCCT 45780

CCGGGGTCTT CGGCTCCGCC GGGCAGGGCA ACTACGCCGC TGCCAACGCC TACCTGGACG 45840

CCGTGGTCCG CAACCGCCGG GCCCGGGGCC TGCCCGGCAC ATCGCTGGCC TGGGGCCTGT 45900

CGCGGTGTGG

GGGAACAGAC CGACGGGATG ACCGCGCACC TCGGCGACGC CGACCAGGCG CGGGCGAGTC 45960

GCGGCGGGGT CCTCGCCATC TCACCCGCCG AAGGCATGGA GCTGTTCGAC GCAGCGCCGG 46020

ACGGGCTCGT CGTCCCGGTC AAGCTGGACC TGC GCAAGAC CCGCGCCGGC GGGACGGTGC 46080

CGCACCTGCT GCGCGGCCCTG GTCCGCCCGG GACGGCAGCA GGCCCGTCCG GCGTCCACTG 46140

TGGACAACGG ACTGGCCGGG CGACTCGCCG GGCTCGCGCC GCGGAGCAG GAGGCGCTGC 46200

TGCTCGACGT CGTCCGCACG CAGGTCGCGC TGGTGCTCGG GCACGCCGGG CCGGAGGCCG 46260

TCCGCGCGGA CACGGCGTTC AAGGACACCG GCTTCGACTC GCTGACGTCG GTGGAAGTGC 46320

GCAACCGGCT GCGCGAGGCG AGCGGGCTGA AGCTGCCCCG GACGCTCGTC TTCGACTACC 46380

CGACGCCGGT CGCGCTGGCC CGCTACCTGC GTGACGAACT CGGCGACACG GTGGCAACAA 46440

CTCCGGTGGC CACCGCGGCC GCAGCGGACG CCGGCGAGCC GATCGCCATC GTCGGCATGG 46500

CGTGCCGGCT GCCGGGCGGG GTCACCGATC CCGAAGGCCT GTGGCGCCTG GTGCGCGACG 46560

GCCTCGAAGG GCTGTCTCCC TTCCCCGAGG ACCGGGGCTG GGACCTGGAG AACCTGTTCG 46620

ACGACGACCC CGACCGCTCC GGCACGACGT ACACCAGCCG GGGCGGGTTC CTCGACGGCG 46680

CCGGCCTGTT CGACGCGGGC TTCTTCGGGA TTTCGCCGCG CGAGGCGCTG GCCATGGACC 46740

CGCAGCAGCG GCTGCTGCTC GAGGCGGCCT GGAAGCCCT CGAAGGCACC GGTGTTCGACC 46800

CGGGCTCGTT GAAGGGCGCC GACGTCGGGG TGTTCCCGG GGTGTCCAAC CAGGGCTATG 46860

GGATGGGCGC GGATCCGGCC GAACTGGCGG GGTACGCGAG CACGGCGGGC GCTTCGAGCG 46920

TCGTCTCGGG CCGAGTCTCG TACGTCTTCG GGTTCGAAGG ACCGGCGGTC ACGATCGACA 46980

CGGCTTGCTC GTCGTCGCTG GTGGCGATGC ACCTGGCCGG GCAGGCGCTG CGGCAGGGCG 47040

AGTGCTCGAT GGCCCTGGCC GGTGGCGTCA CGGTGATGGG GACGCCCCGC ACGTTCGTGG 47100

AGTTCGCGAA GCAGCGCGGC CTGGCCGGCG ACGGCCGGTG CAAGGCCTAC GCCGAAGGCG 47160

CGGACGGCAC GGGCTGGGCC GAGGGCGTCG GGGTCGTCGT GCTGGAGCGG CTGTCGGTGG 47220

CGCGCGAGCG CGGGCACC GG GTGCTGGCCG TGCTGCGCGG CAGCGCGGTC AACTCCGACG 47280

GCGCGTCCAA CGGCCTGACC GCCCCAACG GGCCGTCGCA GCAACGGGTG ATCCGCCGGG 47340

CCCTGGCCGG CGCCGGCCTC GAACCGTCCG ATGTGGACAT CGTGAAGGG CACGGCACCG 47400

GGACGGCGCT GGGCGACCCG ATCGAGGCGC AGGCCCTGCT GGCCACCTAC GGCAAGGACC 47460

GCGACCCGGA GACGCCGTTG TGGCTGGGGT CGGTGAAGTC GAACTTCGGC CACACGCAGT 47520

CCGCGGCCGG CGTGGCCGGG GTGATCAAGA TGGTGCAGGC GCTGCGCCAC GGCATCATGC 47580

CGCCACCCT GCACGTGGAC CGGCCACCA GCCAGGTCGA CTGGTCCGCG GGGGCCGTCG 47640

AAGTGCTGAC CGAGGCACGG GAGTGGCCGC GGAACGGCCG TCCGCGCCGG GCCGGGGTGT 47700

CCTCGTTCGG GATCAGCGGC ACGAACGCC ACCTGATCAT CGAAGAAGCA CCGGCCGAGC 47760

CACAGCTTGC CGGACCACCG CCGGACGGCG GTGTGGTGCC GCTGGTCGTC TCGGCTCGCA 47820

GCCCCGGTGC CCTGGCCGGT CAGGCGCGTC GGCTGGCCAC GTTCTCGGC GACGGGCCCC 47880

TTTCCGACGT CGCCGGTGCG CTGACGAGCC GCGCCCTGTT CGGCGAGCGC GCGGTGTCG 47940

TGGCGGATTC GGCCGAGGAA GCCCGCGCCG GTCTGGGCGC ACTGGCCCGC GGCGAAGACG 48000

CGCCGGGCCT GGTCCGCGGC CGGGTGCCCG CGTCCGGCCT GCCGGGCAAG CTCGTGTGGG 48060

TGTTCCCCGG GCAGGGGACG CAGTGGGTGG GCATGGGCCG CGAACTCCTC GAAGAGTCTC 48120

2025052404

CGGTGTTTCG CGAGCGGATC GCCGAGTGTG CGGCCGCGCT GGAGCCGTGG ATCGGCTGGT 48180

CGCTGTTTGA CGTCTCCGT GGCACGGTG ACCTCGATCG GGTCGATGTG CTGCAGCCCG 48240

CGTGCTTTGC GGTGATGGTC GGCTTGCCCG CGGTGTGGTC CTCGGCCGGG GTGGTCCCCG 48300

ATGCGGTGCT CGGCCACTCC CAGGGTGAGA TCGCCGCGGC GTGCGTGTG GGTGCGTTGT 48360

CGCTGGAGGA TCGGGCGAAG GTGGTTGCCC TGCGCAGCCA GGCCATCGCC GCGAAGCTCT 48420

CCGGCCGCGG CGGGATGGCT TCGGTGCGCT TGGGCGAAGC CGATGTGGTG TCGCGGCTGG 48480

CGGACGGGGT CGAGGTGGCT GCCGTCAACG GTCCGGCGTC CGTGGTGATC GCGGGGGATG 48540

CCCAGGCCCT CGACGAAACG CTGGAAGCGC TGTCCGGTGC GCGAATCCGG GCTCGGCGGG 48600

TGGCGGTGGA CTACGCCTCG CACACCCGGC ACGTCGAAGA CATCGAAGAC ACCCTCGCCG 48660

AAGCGCTGGC CGGGATCGAC GCCCGGGCGC CGCTGGTGCC GTTCTCTTCC ACCCTCACC 48720

GCGAGTGGAT CCGGGACGAG GCGCTCGTGG ACGGCGGCTA CTGGTACCGG AACCTGCGCG 48780

GCCGGGTGCG GTTCGGCCCG GCCGTCGAGG CGCTGCTGGC CCAGGGGCAC GGTGTGTTTCG 48840

TCGAGCTCAG CGCCACCCG GTGCTGGTCC AGCCGATCAC CGAGCTCACC GACGAAACCG 48900

CCGCCGTCGT CACCGGTTTCG CTCGCGCGG ACGACGGTGG CCTGCGCCGG CTGCTGACCT 48960

CGATG3CCGA GCTCTTCGTC CGTGGGGTTCG AAGTGGACTG GACGTCGCTG GTGCCGCCGG 49020

CCCGGGCCGA CCTCCCGACG TACGCCTTCG ACCACGAGCA CTACTGGCTC CGCGCCGCGG 49080

ACACCGCTTC CGACGCGGTC TCGCTGGGGC TGGCCGGGGC GGACCACCCG CTGCTCGGCG 49140

CGGTGCTGCA GCTTCCGCG TCCGACGGCC TGGTCTTCAC TTCCCGGCTC TCCCTGCGCT 49200

CGCACCCCTG GCTGGCCGAC CACGCGGTCC GGGACGTCGT GATCGTCCCC GGCACCGGGC	49260
TGGTCGAGCT GGCCGTGCGG GCCGGTGACG AAGCCGGCTG CCCGGTGCTC GACGAGCTGG	49320
TGATCGAGGC GCCGCTCGTG GTGCCCCGCC GCGGCGGGGT CCGCGTGCAG GTCGCCCTCG	49380
GCGGCCCCGC CGACGACGGT TCGCGCACGG TGGACGTCTT CTCCTTGCGC GAAGACGCGG	49440
ACAGCTGGCT CCGGCACGCC ACGGGCGTGC TGGTCCCGGA GAACCGGCCG CGGGGGACCG	49500
CCGCGTTCGA CTTCGCCGCC TGGCCGCCAC CGGAGGCGAA GCCCCTGGAC CTCACCGGTG	49560
CCTACGACGT GCTCGCGGAC GTCGGGTACG GCTACGGGCC CACGTTCCGG GCCGTGCGGG	49620
CCGTGTGGCG GCGCGGCAGC GGAACACCA CCGAGACCTT CGCCGAGATC GCCCTGCCCC	49680
AAGACGCCCG CGCGGAAGCC GGCCGGTTCG GCATCCACCC CGCGCTGCTG GACGCGGCCC	49740
TGCACTCGAC GATGGTCAGC GCCGCGGCGG ACACCGAGTC CTACGGCGAC GAAGTGCGGC	49800
TGCCGTTCGC GTGGAACGGG CTGCGGCTGC ACGCGGCCGG CGCCTCGGTG CTGCGGTGC	49860
GCGTCGCCAA GCCCGAGCGG GACAGTCTGT CGCTGGAGGC CGTCGACGAG TCCGGCGGCC	49920
TGTCGTGAC GCTGGATTCC CTGGTCGGGC GCCCGGTGTC GAACGACCAG CTGACGACGG	49980
CGGCGGGGCC GCGGGGCGCC GGCTCGCTGT ACCGCGTGGA CTGGACGCCA TTGTCCTCAG	50040
TGGACACTTC GGGACGGGTG CCGTCCTGGC TTCCGGTCGC CACCGCGGAA GAGGTGGCGA	50100
CGCTGGCCGA CGACGTCCTG ACCGGCGCGA CCGAGGCGCC GGCGGTGGCC GTCATGGAGG	50160
CCGTCGCCGA CGAGGGTTCC GTGCTGGCGC TCACCGTCCG GGTGCTGGAC GTGGTCCAGT	50220
GCTGGCTGGC CGGCGGCGGG CTGGAGGGGA CGAAGCTCGC GATCGTGACC CGCGGCGCGG	50280
TGCCCCCGGG CGACGGCGTG GTGCACGACC CGGCCGCGC CGCGGTGTGG GGGCTGGTCC	50340

GGGCCGCGCA GGC GGAGAAC CCGGACCGGA TCGTCTCCT CGACGTCGAG CCGGAAGCCG 50400

ACGTACCGCC GCTGCTGGGT TCGGTGCTCG CCGACGGCGA GCCGCAGGTC GCGGTGCGCG 50460

GAACCACGCT GTCCATCCCC CGCCTCGCCC GCGCCGCCCG GCCCGACCCG GCCGCCGGGT 50520

TCAAGACCCG GGGACCGGTG CTGGTCACCG GCGGGACCGG GTCGCTCGGC GGCCTGGTCG 50580

CCCGGCACCT GGTGAGCGG CACGGCGTCC GGCAGCTGGT GCTGGCGAGT CGCCGGGGCC 50640

TGGACGCCGA AGGCGCGAAG GACCTGGTCA CCGACCTCAC CGCACTGGGG GCCGACGTCG 50700

CGGTGCCCCC TTGCGACGTC GCCGACCGGG ACCAGGTGGC GGCCCTGCTG ACCGAGCACC 50760

GGCCGTCCGC CGTGGTGAC ACGGCCGGCG TCCCGGACGC CGGGGTGATC GGGACGGTGA 50820

CCCCGGACCG GCTGGCCGAG GTGTTCGCGC CCAAGGTCAC CGCGGCCCGG CACCTCGACG 50880

AGCTGACCCG CGACCTGGAC CTCGACAGTT TCGTCGTCTA CTCCTCGGTT TCCGCGGTGT 50940

TCATGGGCGC CGGCAGCGGC AGCTACGCCG CGGCGAACGC GTACCTGGAC GGGCTGATGG 51000

CCCACCGGCG CGCGGCCGGC CTGCCGGGCC AGTCGCTGGC GTGGGGGCTG TGGGACCAGA 51060

CCACCGGCGG CATGGCGGCC GGGACCGACG AGGCCGGCCG GGCCCGGATG ACCCGGCGCG 51120

GCGGCCTGGT CGCGATGAAA CCCGCCGCCG GACTGGACCT CTTGACGCT GCCATCGGGT 51180

CCGGCGAGCC GCTGCTGGTG CCCGCCAGC TCGACCTGCG GGGCCTGCGC GCCGAAGCGG 51240

CGGGCGGCAC CGAAGTGCCG CACCTGCTGC GCGGCCTGGT CCGCGCCGGA CGCCAGCAGG 51300

CCCGTGCGGC GTCCACTGTG GAGGAGAACT GGGCCGGCCG GCTGGCCGGG CTCGAGCCGG 51360

CCGAGCGGGG CCAGGTCTC CTGGAAGTGG TCGCGGCCCA GGTGGCAGGG GTCCTGGGCT 51420

ACCGCGCCGC CCACCAGGTC GACCCGGACC AGGGCCTGTT CGAGATCGGG TTCGACTCGC 51480

TCACCGCGAT CGAACTCCGC AACCGGCTGC GCGCCAGGAC CGAACGGAAG ATCTCGCCCG 51540

GTGTCGTCTT CGACCATCCC ACGCCGGCCC TGCTCGCCGC GCACCTGAAC GAGCTGCTCC 51600

GAAAGAAGGT GTGAACGTGT TCGACGTGGA GACCTACCTC CAGCGGATCG GCTGCGGCGG 51660

GGAAACCGGC GTGGACCTCG AAACGCTGGC GAAGCTGCAG AAGAGCCACC TGATGGCGAT 51720

CCCGTACAGC AGCCTCGCCT ACGAACTCCG GGACGCGGTG AACGTCGTCTG ACCTCGACGA 51780

GGACGACGTC TTCGTCACCA GCATCGCCGA AGGGCAGGGC GGCGCCTGCT ACCACCTGAA 51840

CCGGCTGTTC CACCGGCTCC TGACCGAACT CGGCTACGAC GTCACGCCGC TGGCCGGCAG 51900

CACCGCCGAA GGCCGGGAGA CCTTCGGCAC CGACGTCGAG CACATGTTCA ACCTGGTCAC 51960

CCTGGACGGC GCCGACTGGC TCGTGGACGT CGGCTACCCC GGCCCCACCT ACGTCGAGCC 52020

ACTGGCGGTC TCGCCCGCGG TGCAGACCCA GTACGGGAGC CAGTTCGGT TGGTGAACA 52080

GGAAACCGGT TATGCGCTGC AACGCCGGG TCGGCTCACC CGCTGGAGCG TCGTCTACAC 52140

G TTCACGACG CAACCGCGTC AGTGGAGTGA CTGGAAGGAA CTGGAGGACA ACTTCGGGGC 52200

CCTCGTGGGG GACACCACCC GCACCGACAC GCAGGAAACC CTGTGCGGCC GCGCGTTCGC 52260

GAACGGCCAG GTCTTCCTGC GGCAGCGCCG CTACCTGACG GTCGAGAACG GCCGCGAGCA 52320

G GTGCGCACG ATCACCAGC ACGACGAGTT CCGGGCGCTG GTGTCCCGCG TGCTGTCCGG 52380

CGACCACGGC TGAAGTGGCG AAAGGCACGA CGATGACGGA AAAAGCGGGC CTGCTGGCGA 52440

AGTTCGCGCG CCTCTGCAAA ACCGCCTACG AGCACCATA CATCCGTAC CTGCACTTCT 52500

TCTACGGCGG CGAGTACCTC CACCACGGCA GCGAGCCGGT GTCCCGGATC GCGGACCTGC 52560

CGTACGTGAC CGTGCCGGAG CCGCGGAAGA AGGCGCCGTG AGGACGACGA TCCCGGTCCG 52620

CCTGGCGGAA CGGTCCCTACG ACGTGCTCGT CGGCCCCGGG GTGCGGGCGG CGCTGCCCCA 52680

GGTCGTCCGG CGGCTCGGCG CGAGACGGGC CGTGGTCGTG TCGGCCCCGC CGGCGGACTG 52740

GGTGCCCCGC ACCGGCGTCG AGACCCTECT GCTCCAGGCG CGCGACGGCG AGCCGACCAA 52800

GCGGCTGTCC ACAGTGGAGG AACTGTGCGG TGAGTTCGCG CGGTTCGGGC TCACCCGGTC 52860

CGACGTCTGTG GTCTCCTGCG GCGGCGGCAC GACCACGGAC GTCGTCTGGC TCGCGGCCG 52920

GCTGTACCAC CGGGGGGTG CCGTGGTCCA CCTGCCCACG TCCCTGCTCG CCCAGGTCGA 52980

CGCCAGCGTC GCGGGAAGA CCGCGGTGAA CCTGCCGGCG GGCAAGAACC TCGTCGGGGC 53040

GTACTGGCAG CCCAGCGCGG TGCTGTGCGA CACGGACTAC CTGACGACGC TGCCGCGGCG 53100

GGAGGTGCTG AACGGCCTCG GCGAGATCGC CCGCTGCCAC TTCATCGGCG CGCCGGACCT 53160

GCGGGGGCGC TCGCGCCCGG AGCAGATCGC CGCCAGCGTC ACCCTCAAGG CGGGCATCGT 53220

CGCGCAGGAC GAGCGGGACA CCGGCCCCGCG GCACCTGCTC AACTACGGCC ACACGCTGGG 53280

GCACGCGCTG GAGATCGCGA CCGGCTTCGC CCTGCGCCAC GCGGAGGCGG TGGCGATCGG 53340

CACGGTCTTC GCGGGCCGGC TGGCCGGCGC GCTCGGCCCG CTCGACCAGT CCGGTGTGGA 53400

CGAACACCTC GCCGTCTCC GCCACTACGG CCTGCCCCGCC GCGCTGCCCCG CGGACGTCEA 53460

CCCCGCGGTG CTCGTCCGCG AGATGTACCG GGACAAGAAG GCGATCACCG GGCTCGCCTT 53520

CGTCCTGGCC GGGCCGCGG GCGCGGAGCT GGTGAGCGAC GTGCCGGCGC CGGTCTGCAC 53580

CGACGTCTTG GACCGGATGC CCCGCGACAG CCTGGAACAC CTGGTGGGGA CGACGGAAGC 53640

GGCGGCGCCG TGAAGCGGCA GCCGGACTTC GCGGCCACG GCCGGGCGGT CGACCGGGTG 53700
CTGGCCGGCC GGCTGAGCGC GGCCTGGCC CGGCCGGCCG CGCAGCAGCC GGGCTGGCCG 53760
GACGCCGAGC GGGCGGCCGA GGTGAATTC 53789

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4572 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Phe Tyr Thr Ser Gly Thr Thr Gly Arg Pro Lys Gly Val Val Ser
1 5 10 15

Thr Gln Arg Asn Cys Leu Trp Ser Val Ala Ser Cys Tyr Val Pro Phe
20 25 30

Pro Gly Leu Ser Asp Gln Asp Arg Val Leu Trp Pro Leu Pro Leu Phe
35 40 45

His Ser Leu Ser His Ile Ala Cys Val Leu Ser Ala Thr Val Val Gly
50 55 60

Ala Ser Val Arg Ile Ala Asp Gly Ser Ser Ala Asp Asp Val Met Arg
65 70 75 80

Leu Ile Glu Ala Glu Ser Ser Thr Phe Leu Ala Gly Val Pro Thr Thr
85 90 95

Tyr His His Leu Val Arg Ala Ala Arg Gln Arg Gly Phe Ser Ala Pro
100 105 110

Ser Leu Arg Ile Gly Leu Ala Gly Gly Ala Val Leu Gly Ala Gly Leu
115 120 125

Arg Ser Glu Phe Glu Glu Thr Phe Gly Val Pro Leu Ile Asp Ala Tyr
130 135 140

Gly Ser Thr Glu Thr Cys Gly Ala Ile Thr Met Asn Pro Pro Asp Gly
145 150 155 160

Ala Arg Val Glu Gly Ser Cys Gly Leu Ala Val Pro Gly Val Asp Val
165 170 175

Arg Val Val Asp Pro Asp Thr Gly Leu Asp Val Pro Ala Gly Glu Glu
180 185 190

Gly Glu Val Trp Val Ser Gly Pro Asn Val Met Leu Gly Tyr His Asn
195 200 205

Ser Pro Glu Ala Thr Ala Ala Ala Met Arg Asp Gly Trp Phe Arg Thr
210 215 220

Gly Asp Leu Ala Arg Arg Asp Asp Ala Gly Tyr Phe Thr Ile Cys Gly
225 230 235 240

Arg Ile Lys Glu Leu Ile Ile Arg Gly Gly Ala Asn Ile His Pro Gly
245 250 255

Glu Val Glu Ala Val Leu Arg Thr Val Asp Gly Val Ala Asp Ala Ala
260 265 270

Val Gly Gly Val Pro His Asp Thr Leu Gly Glu Val Pro Val Ala Tyr
275 280 285

Val Ile Pro Gly Pro Thr Gly Phe Asp Pro Ala Ala Leu Ile Glu Lys
290 295 300

Cys Arg Glu Gln Leu Ser Ala Tyr Lys Val Pro Asp Arg Ile Leu Glu
305 310 315 320

Val Ala His Ile Pro Arg Thr Ala Ser Gly Lys Ile Arg Arg Gly Leu
325 330 335

Leu Thr Asp Glu Pro Ala Gln Leu Arg Tyr Ala Ala Thr Glu His Glu
340 345 350

Glu Gln Ser Arg His Ala Asp Glu Ser Val Ala Ala Ala Leu Arg Ala
355 360 365

Arg Leu Ser Gly Leu Asp Glu Arg Ala Gln Cys Glu Leu Leu Glu Asp
370 375 380

Leu Val Arg Thr Gln Ala Ala Asp Val Leu Gly Gln Pro Val Pro Asp
385 390 395 400

Gly Arg Ala Phe Arg Asp Leu Gly Phe Thr Ser Leu Ala Ile Val Glu
405 410 415

Leu Arg Asn Arg Leu Thr Glu His Thr Gly Leu Trp Leu Pro Ala Ser
420 425 430

Ala Val Phe Asp His Pro Thr Pro Ala Ala Leu Ala Ala Arg Val Arg
435 440 445

Ala Glu Leu Leu Gly Ile Thr Gln Ala Val Ala Glu Pro Val Val Ala
450 455 460

Ala Asp Pro Gly Glu Pro Ile Ala Ile Val Gly Met Ala Cys Arg Leu

206600" 533400"

465 470 475 480
Pro Gly Gly Val Ala Ser Pro Glu Asp Leu Trp Arg Leu Val Ala Glu
 485 490 495
Arg Val Asp Ala Val Ser Glu Phe Pro Gly Asp Arg Gly Trp Asp Leu
 500 505 510
Asp Ser Leu Ile Asp Pro Asp Arg Glu Arg Ala Gly Thr Ser Tyr Val
 515 520 525
Gly Gln Gly Gly Phe Leu His Asp Ala Gly Glu Phe Asp Ala Gly Phe
 530 535 540
Phe Gly Ile Ser Pro Arg Glu Ala Val Ala Met Asp Pro Gln Gln Arg
545 550 555 560
Leu Leu Leu Glu Thr Ser Trp Glu Ala Leu Glu Asn Ala Gly Val Asp
 565 570 575
Pro Ile Ala Leu Lys Gly Thr Asp Thr Gly Val Phe Ser Gly Leu Met
 580 585 590
Gly Gln Gly Tyr Gly Ser Gly Ala Val Ala Pro Glu Leu Glu Gly Phe
 595 600 605
Val Thr Thr Gly Val Ala Ser Ser Val Ala Ser Gly Arg Val Ser Tyr
 610 615 620
Val Leu Gly Leu Glu Gly Pro Ala Val Thr Val Asp Thr Ala Cys Ser
625 630 635 640
Ser Ser Leu Val Ala Met His Leu Ala Ala Gln Ala Leu Arg Gln Gly
 645 650 655
Glu Cys Ser Met Ala Leu Ala Gly Gly Val Thr Val Met Ala Thr Pro
 660 665 670

2060303 "S E 4400"

Gly Ser Phe Val Glu Phe Ser Arg Gln Arg Ala Leu Ala Pro Asp Gly
675 680 685

Arg Cys Lys Ala Phe Ala Ala Ala Ala Asp Gly Thr Gly Trp Ser Glu
690 695 700

Gly Val Gly Val Val Val Leu Glu Arg Leu Ser Val Ala Arg Glu Arg
705 710 715 720

Gly His Arg Ile Leu Ala Val Leu Arg Gly Ser Ala Val Asn Gln Asp
725 730 735

Gly Ala Ser Asn Gly Leu Thr Ala Pro Asn Gly Leu Ser Gln Gln Arg
740 745 750

Val Ile Arg Arg Ala Leu Ala Ala Ala Gly Leu Ala Pro Ser Asp Val
755 760 765

Asp Val Val Glu Ala His Gly Thr Gly Thr Thr Leu Gly Asp Pro Ile
770 775 780

Glu Ala Gln Ala Leu Leu Ala Thr Tyr Gly Gln Glu Arg Lys Gln Pro
785 790 795 800

Leu Trp Leu Gly Ser Leu Lys Ser Asn Ile Gly His Ala Gln Ala Ala
805 810 815

Ala Gly Val Ala Gly Val Ile Lys Met Val Gln Ala Leu Arg His Glu
820 825 830

Thr Leu Pro Pro Thr Leu His Val Asp Lys Pro Thr Leu Glu Val Asp
835 840 845

Trp Ser Ala Gly Ala Ile Glu Leu Leu Thr Glu Ala Arg Ala Trp Pro
850 855 860

Arg Asn Gly Arg Pro Arg Arg Ala Gly Val Ser Ser Phe Gly Val Ser
865 870 875 880

Gly Thr Asn Ala His Leu Ile Leu Glu Glu Ala Pro Ala Glu Glu Pro
885 890 895

Val Ala Ala Pro Glu Leu Pro Val Val Pro Leu Val Val Ser Ala Arg
900 905 910

Ser Thr Glu Ser Leu Ser Gly Gln Ala Glu Arg Leu Ala Ser Leu Leu
915 920 925

Glu Gly Asp Val Ser Leu Thr Glu Val Ala Gly Ala Leu Val Ser Arg
930 935 940

Arg Ala Val Leu Asp Glu Arg Ala Val Val Val Ala Gly Ser Arg Glu
945 950 955 960

Glu Ala Val Thr Gly Leu Arg Ala Leu Asn Thr Ala Gly Ser Gly Thr
965 970 975

Pro Gly Lys Val Val Trp Val Phe Pro Gly Gln Gly Thr Gln Trp Ala
980 985 990

Gly Met Gly Arg Glu Leu Leu Ala Glu Ser Pro Val Phe Ala Glu Arg
995 1000 1005

Ile Ala Glu Cys Ala Ala Ala Leu Ala Pro Trp Ile Asp Trp Ser Leu
1010 1015 1020

Val Asp Val Leu Arg Gly Glu Gly Asp Leu Gly Arg Val Asp Val Leu
1025 1030 1035 1040

Gln Pro Ala Cys Phe Ala Val Met Val Gly Leu Ala Ala Val Trp Glu
1045 1050 1055

Ser Val Gly Val Arg Pro Asp Ala Val Val Gly His Ser Gln Gly Glu

[illegible]

Thr Leu Arg Arg Glu Asp Gly Gly Leu Arg Arg Leu Leu Ala Ser Met
1265 1270 1275 1280

Gly Glu Leu Phe Val Arg Gly Ile Asp Val Asp Trp Thr Ala Met Val
1285 1290 1295

Pro Ala Ala Gly Trp Val Asp Leu Pro Thr Tyr Ala Phe Glu His Arg
1300 1305 1310

His Tyr Trp Leu Glu Pro Ala Glu Pro Ala Ser Ala Gly Asp Pro Leu
1315 1320 1325

Leu Gly Thr Val Val Ser Thr Pro Gly Ser Asp Arg Leu Thr Ala Val
1330 1335 1340

Ala Gln Trp Ser Arg Arg Ala Gln Pro Trp Ala Val Asp Gly Leu Val
1345 1350 1355 1360

Pro Asn Ala Ala Leu Val Glu Ala Ala Ile Arg Leu Gly Asp Leu Ala
1365 1370 1375

Gly Thr Pro Val Val Gly Glu Leu Val Val Asp Ala Pro Val Val Leu
1380 1385 1390

Pro Arg Arg Gly Ser Arg Glu Val Gln Leu Ile Val Gly Glu Pro Gly
1395 1400 1405

Glu Gln Arg Arg Arg Pro Ile Glu Val Phe Ser Arg Glu Ala Asp Glu
1410 1415 1420

Pro Trp Thr Arg His Ala His Gly Thr Leu Ala Pro Ala Ala Ala Ala
1425 1430 1435 1440

Val Pro Glu Pro Ala Ala Ala Gly Asp Ala Thr Asp Val Thr Val Ala
1445 1450 1455

Gly Leu Arg Asp Ala Asp Arg Tyr Gly Ile His Pro Ala Leu Leu Asp
1460 1465 1470

Ala Ala Val Arg Thr Val Val Gly Asp Asp Leu Leu Pro Ser Val Trp
1475 1480 1485

Thr Gly Val Ser Leu Leu Ala Ser Gly Ala Thr Ala Val Thr Val Thr
1490 1495 1500

Pro Thr Ala Thr Gly Leu Arg Leu Thr Asp Pro Ala Gly Gln Pro Val
1505 1510 1515 1520

Leu Thr Val Glu Ser Val Arg Gly Thr Pro Phe Val Ala Glu Gln Gly
1525 1530 1535

Thr Thr Asp Ala Leu Phe Arg Val Asp Trp Pro Glu Ile Pro Leu Pro
1540 1545 1550

Thr Ala Glu Thr Ala Asp Phe Leu Pro Tyr Glu Ala Thr Ser Ala Glu
1555 1560 1565

Ala Thr Leu Ser Ala Leu Gln Ala Trp Leu Ala Asp Pro Ala Glu Thr
1570 1575 1580

Arg Leu Ala Val Val Thr Gly Asp Cys Thr Glu Pro Gly Ala Ala Ala
1585 1590 1595 1600

Ile Trp Gly Leu Val Arg Ser Ala Gln Ser Glu His Pro Gly Arg Ile
1605 1610 1615

Val Leu Ala Asp Leu Asp Asp Pro Ala Val Leu Pro Ala Val Val Ala
1620 1625 1630

Ser Gly Glu Pro Gln Val Arg Val Arg Asn Gly Val Ala Ser Val Pro
1635 1640 1645

Arg Leu Thr Arg Val Thr Pro Arg Gln Asp Ala Arg Pro Leu Asp Pro

1650	1655	1660	
Glu Gly Thr Val Leu Ile Thr Gly Gly Thr Gly Thr Leu Gly Ala Leu			
1665	1670	1675	1680
Thr Ala Arg His Leu Val Thr Ala His Gly Val Arg His Leu Val Leu			
1685	1690	1695	
Val Ser Arg Arg Gly Glu Ala Pro Glu Leu Gln Glu Glu Leu Thr Ala			
1700	1705	1710	
Leu Gly Ala Ser Val Ala Ile Ala Ala Cys Asp Val Ala Asp Arg Ala			
1715	1720	1725	
Gln Leu Glu Ala Val Leu Arg Ala Ile Pro Ala Glu His Pro Leu Thr			
1730	1735	1740	
Ala Val Ile His Thr Ala Gly Val Leu Asp Asp Gly Val Val Thr Glu			
1745	1750	1755	1760
Leu Thr Pro Asp Arg Leu Ala Thr Val Arg Arg Pro Lys Val Asp Ala			
1765	1770	1775	
Ala Arg Leu Leu Asp Glu Leu Thr Arg Glu Ala Asp Leu Ala Ala Phe			
1780	1785	1790	
Val Leu Phe Ser Ser Ala Ala Gly Val Leu Gly Asn Pro Gly Gln Ala			
1795	1800	1805	
Gly Tyr Ala Ala Ala Asn Ala Glu Leu Asp Ala Leu Ala Arg Gln Arg			
1810	1815	1820	
Asn Ser Leu Asp Leu Pro Ala Val Ser Ile Ala Trp Gly Tyr Trp Ala			
1825	1830	1835	1840
Thr Val Ser Gly Met Thr Glu His Leu Gly Asp Ala Asp Leu Arg Arg			
1845	1850	1855	

Asn Gln Arg Ile Gly Met Ser Gly Leu Pro Ala Asp Glu Gly Met Ala
1860 1865 1870

Leu Leu Asp Ala Ala Ile Ala Thr Gly Gly Thr Leu Val Ala Ala Lys
1875 1880 1885

Phe Asp Val Ala Ala Leu Arg Ala Thr Ala Lys Ala Gly Gly Pro Val
1890 1895 1900

Pro Pro Leu Leu Arg Gly Leu Ala Pro Leu Pro Arg Arg Ala Ala Ala
1905 1910 1915 1920

Lys Thr Ala Ser Leu Thr Glu Arg Leu Ala Gly Leu Ala Glu Thr Glu
1925 1930 1935

Gln Ala Ala Ala Leu Leu Asp Leu Val Arg Arg His Ala Ala Glu Val
1940 1945 1950

Leu Gly His Ser Gly Ala Glu Ser Val His Ser Gly Arg Thr Phe Lys
1955 1960 1965

Asp Ala Gly Phe Asp Ser Leu Thr Ala Val Glu Leu Arg Asn Arg Leu
1970 1975 1980

Ala Ala Ala Thr Gly Leu Thr Leu Ser Pro Ala Met Ile Phe Asp Tyr
1985 1990 1995 2000

Pro Lys Pro Pro Ala Leu Ala Asp His Leu Arg Ala Lys Leu Phe Gly
2005 2010 2015

Ser Ala Ala Asn Arg Pro Ala Glu Ile Gly Thr Ala Ala Ala Glu Glu
2020 2025 2030

Pro Ile Ala Ile Val Ala Met Ala Cys Arg Phe Pro Gly Gly Val His
2035 2040 2045

Ser Pro Glu Asp Leu Trp Arg Leu Val Ala Asp Gly Ala Asp Ala Val
2050 2055 2060

Thr Glu Phe Pro Ala Asp Arg Gly Trp Asp Thr Asp Arg Leu Tyr His
2065 2070 2075 2080

Glu Asp Pro Asp His Glu Gly Thr Thr Tyr Val Arg His Gly Ala Phe
2085 2090 2095

Leu Asp Asp Ala Ala Gly Phe Asp Ala Ala Phe Phe Gly Ile Ser Pro
2100 2105 2110

Asn Glu Ala Leu Ala Met Asp Pro Gln Gln Arg Leu Leu Leu Glu Thr
2115 2120 2125

Ser Trp Glu Leu Phe Glu Arg Ala Ala Ile Asp Pro Thr Thr Leu Ala
2130 2135 2140

Gly Gln Asp Ile Gly Val Phe Ala Gly Val Asn Ser His Asp Tyr Ser
2145 2150 2155 2160

Met Arg Met His Arg Ala Ala Gly Val Glu Gly Phe Arg Leu Thr Gly
2165 2170 2175

Gly Ser Ala Ser Val Leu Ser Gly Arg Val Ala Tyr His Phe Gly Val
2180 2185 2190

Glu Gly Pro Ala Val Thr Val Asp Thr Ala Cys Ser Ser Ser Leu Val
2195 2200 2205

Ala Leu His Met Ala Val Gln Ala Leu Gln Arg Gly Glu Cys Ser Met
2210 2215 2220

Ala Leu Ala Gly Gly Val Met Val Met Gly Thr Val Glu Thr Phe Val
2225 2230 2235 2240

Glu Phe Ser Arg Gln Arg Gly Leu Ala Pro Asp Gly Arg Cys Lys Ala

2050 2055 2060 2065 2070 2075 2080 2085 2090 2095 2100 2105 2110 2115 2120 2125 2130 2135 2140 2145 2150 2155 2160 2165 2170 2175 2180 2185 2190 2195 2200 2205 2210 2215 2220 2225 2230 2235 2240

2245	2250	2255
Phe Ala Asp Gly Ala Asp Gly Thr Gly Trp Ser Glu Gly Val Gly Leu		
2260	2265	2270
Leu Leu Val Glu Arg Leu Ser Glu Ala Gln Arg Arg Gly His Gln Val		
2275	2280	2285
Leu Ala Val Val Arg Gly Ser Ala Val Asn Ser Asp Gly Ala Ser Asn		
2290	2295	2300
Gly Leu Thr Ala Pro Asn Gly Pro Ser Gln Gln Arg Val Ile Arg Lys		
2305	2310	2315 2320
Ala Leu Ala Ala Ala Gly Leu Ser Thr Ser Asp Val Asp Ala Val Glu		
2325	2330	2335
Ala His Gly Thr Gly Thr Thr Leu Gly Asp Pro Ile Glu Ala Glu Ala		
2340	2345	2350
Leu Leu Ala Thr Tyr Gly Gln Asn Arg Glu Thr Pro Leu Trp Leu Gly		
2355	2360	2365
Ser Val Lys Ser Asn Leu Gly His Thr Gln Ala Ala Ala Gly Val Ala		
2370	2375	2380
Gly Val Ile Lys Met Val Met Ala Met Arg His Gly Val Leu Pro Arg		
2385	2390	2395 2400
Thr Leu His Val Asp Arg Pro Ser Ser Tyr Val Asp Trp Ser Ala Gly		
2405	2410	2415
Ala Val Glu Leu Leu Thr Glu Ala Arg Asp Trp Val Ser Asn Gly His		
2420	2425	2430
Pro Arg Arg Ala Gly Val Ser Ser Phe Gly Ile Gly Gly Thr Asn Ala		
2435	2440	2445

His Val Val Leu Glu Glu Val Ala Ala Pro Ile Thr Thr Pro Gln Pro
2450 2455 2460

Glu Pro Ala Glu Phe Leu Val Pro Val Leu Val Ser Ala Arg Thr Ala
2465 2470 2475 2480

Ala Gly Leu Arg Gly Gln Ala Gly Arg Leu Ala Ala Phe Leu Gly Asp
2485 2490 2495

Arg Thr Asp Val Arg Val Pro Asp Ala Ala Tyr Ala Leu Ala Thr Thr
2500 2505 2510

Arg Ala Gln Leu Asp His Arg Ala Val Val Leu Ala Ser Asp Arg Ala
2515 2520 2525

Gln Leu Cys Ala Asp Leu Ala Ala Phe Gly Ser Gly Val Val Thr Gly
2530 2535 2540

Thr Pro Val Asp Gly Lys Leu Ala Val Leu Phe Thr Gly Gln Gly Ser
2545 2550 2555 2560

Gln Trp Ala Gly Met Gly Arg Glu Leu Ala Glu Thr Phe Pro Val Phe
2565 2570 2575

Arg Asp Ala Phe Glu Ala Ala Cys Glu Ala Val Asp Thr His Leu Arg
2580 2585 2590

Glu Arg Pro Leu Arg Glu Val Val Phe Asp Asp Ser Ala Leu Leu Asp
2595 2600 2605

Gln Thr Met Tyr Thr Gln Gly Ala Leu Phe Ala Val Glu Thr Ala Leu
2610 2615 2620

Phe Arg Leu Phe Glu Ser Trp Gly Val Arg Pro Gly Leu Leu Ala Gly
2625 2630 2635 2640

His Ser Ile Gly Glu Leu Ala Ala Ala His Val Ser Gly Val Leu Asp
2645 2650 2655

Leu Ala Asp Ala Gly Glu Leu Val Ala Ala Arg Gly Arg Leu Met Gln
2660 2665 2670

Ala Leu Pro Ala Gly Gly Ala Met Val Ala Val Gln Ala Thr Glu Asp
2675 2680 2685

Glu Val Ala Pro Leu Leu Asp Gly Thr Val Cys Val Ala Ala Val Asn
2690 2695 2700

Gly Pro Asp Ser Val Val Leu Ser Gly Thr Glu Ala Ala Val Leu Ala
2705 2710 2715 2720

Val Ala Asp Glu Leu Ala Gly Arg Gly Arg Lys Thr Arg Arg Leu Ala
2725 2730 2735

Val Ser His Ala Phe His Ser Pro Leu Met Glu Pro Met Leu Asp Asp
2740 2745 2750

Phe Arg Ala Val Ala Glu Arg Leu Thr Tyr Arg Ala Gly Ser Leu Pro
2755 2760 2765

Val Val Ser Thr Leu Thr Gly Glu Leu Ala Ala Leu Asp Ser Pro Asp
2770 2775 2780

Tyr Trp Val Gly Gln Val Arg Asn Ala Val Arg Phe Ser Asp Ala Val
2785 2790 2795 2800

Thr Ala Leu Gly Ala Gln Gly Ala Ser Thr Phe Leu Glu Leu Gly Pro
2805 2810 2815

Gly Gly Ala Leu Ala Ala Met Ala Leu Gly Thr Leu Gly Gly Pro Glu
2820 2825 2830

Gln Ser Cys Val Ala Thr Leu Arg Lys Asn Gly Ala Glu Val Pro Asp

2835	2840	2845
Val Leu Thr Ala Leu Ala Glu Leu His Val Arg Gly Val Gly Val Asp		
2850	2855	2860
Trp Thr Thr Val Leu Asp Glu Pro Ala Thr Ala Val Gly Thr Val Leu		
2865	2870	2875 2880
Pro Thr Tyr Ala Phe Gln His Gln Arg Phe Trp Val Asp Val Asp Glu		
2885	2890	2895
Thr Ala Ala Val Ser Val Thr Pro Pro Pro Ala Glu Pro Ile Val Asp		
2900	2905	2910
Arg Pro Val Gln Asp Val Leu Glu Leu Val Arg Glu Ser Ala Ala Val		
2915	2920	2925
Val Leu Gly His Arg Asp Ala Gly Ser Phe Asp Leu Asp Arg Ser Phe		
2930	2935	2940
Lys Asp His Gly Phe Asp Ser Leu Ser Ala Val Lys Leu Arg Asn Arg		
2945	2950	2955 2960
Leu Arg Asp Phe Thr Gly Val Glu Leu Pro Ser Thr Leu Ile Phe Asp		
2965	2970	2975
Tyr Pro Asn Pro Ala Val Leu Ala Asp His Leu Arg Ala Glu Leu Leu		
2980	2985	2990
Gly Glu Arg Pro Ala Ala Pro Ala Pro Val Thr Arg Asp Val Ser Asp		
2995	3000	3005
Glu Pro Ile Ala Ile Val Gly Met Ser Thr Arg Leu Pro Gly Gly Ala		
3010	3015	3020
Asp Ser Pro Glu Glu Leu Trp Lys Leu Val Ala Glu Gly Arg Asp Ala		
3025	3030	3035 3040

Val Ser Gly Phe Pro Val Asp Arg Gly Trp Asp Leu Asp Gly Leu Tyr
3045 3050 3055

His Pro Asp Pro Ala His Ala Gly Thr Ser Tyr Thr Arg Ser Gly Gly
3060 3065 3070

Phe Leu His Asp Ala Ala Gln Phe Asp Ala Gly Leu Phe Gly Ile Ser
3075 3080 3085

Pro Arg Glu Ala Leu Ala Met Asp Pro Gln Gln Arg Leu Leu Leu Glu
3090 3095 3100

Thr Ser Trp Glu Ala Leu Glu Arg Ala Gly Val Asp Pro Leu Ser Ala
3105 3110 3115 3120

Arg Gly Ser Asp Val Gly Val Phe Thr Gly Ile Val His His Asp Tyr
3125 3130 3135

Val Thr Arg Leu Arg Glu Val Pro Glu Asp Val Gln Gly Tyr Thr Met
3140 3145 3150

Thr Gly Thr Ala Ser Ser Val Ala Ser Gly Arg Val Ala Tyr Val Phe
3155 3160 3165

Gly Phe Glu Gly Pro Ala Val Thr Val Asp Thr Ala Cys Ser Ser Ser
3170 3175 3180

Leu Val Ala Met His Leu Ala Ala Gln Ala Leu Arg Gln Gly Glu Cys
3185 3190 3195 3200

Ser Met Ala Leu Ala Gly Gly Ala Thr Val Met Ala Ser Pro Asp Ala
3205 3210 3215

Phe Leu Glu Phe Ser Arg Gln Arg Gly Leu Ser Ala Asp Gly Arg Cys
3220 3225 3230

Lys Ala Tyr Ala Glu Gly Ala Asp Gly Thr Gly Trp Ala Glu Gly Val
3235 3240 3245

Gly Val Val Val Leu Glu Arg Leu Ser Val Ala Arg Glu Arg Gly His
3250 3255 3260

Arg Val Leu Ala Val Leu Arg Gly Ser Ala Val Asn Gln Asp Gly Ala
3265 3270 3275 3280

Ser Asn Gly Leu Thr Ala Pro Asn Gly Pro Ser Gln Gln Arg Val Ile
3285 3290 3295

Arg Gly Ala Leu Ala Ser Ala Gly Leu Ala Pro Ser Asp Val Asp Val
3300 3305 3310

Val Glu Gly His Gly Thr Gly Thr Ala Leu Gly Asp Pro Ile Glu Val
3315 3320 3325

Gln Ala Leu Leu Ala Thr Tyr Gly Gln Glu Arg Glu Gln Pro Leu Trp
3330 3335 3340

Leu Gly Ser Leu Lys Ser Asn Leu Gly His Thr Gln Ala Ala Ala Gly
3345 3350 3355 3360

Val Val Gly Val Ile Lys Met Ile Met Ala Met Arg His Gly Val Met
3365 3370 3375

Pro Ala Thr Leu His Val Asp Glu Arg Thr Ser Gln Val Asp Trp Ser
3380 3385 3390

Ala Gly Ala Ile Glu Val Leu Thr Glu Ala Arg Glu Trp Pro Arg Thr
3395 3400 3405

Gly Arg Pro Arg Arg Ala Gly Val Ser Ser Phe Gly Ala Ser Gly Thr
3410 3415 3420

Asn Ala His Leu Ile Ile Glu Glu Gly Pro Ala Glu Glu Ala Val Asp

3425	3430	3435	3440
Glu Glu Val Ala Ser Val Val Pro Leu Val Val Ser Ala Arg Ser Ala			
	3445	3450	3455
Gly Ser Leu Ala Gly Gln Ala Gly Arg Leu Ala Ala Val Leu Glu Asn			
	3460	3465	3470
Glu Ser Leu Ala Gly Val Ala Gly Ala Leu Val Ser Gly Arg Ala Thr			
	3475	3480	3485
Leu Asn Glu Arg Ala Val Val Ile Ala Gly Ser Arg Asp Glu Ala Gln			
	3490	3495	3500
Asp Gly Leu Gln Ala Leu Ala Arg Gly Glu Asn Ala Pro Gly Val Val			
3505	3510	3515	3520
Thr Gly Thr Ala Gly Lys Pro Gly Lys Val Val Trp Val Phe Pro Gly			
	3525	3530	3535
Gln Gly Ser Gln Trp Met Gly Met Gly Arg Asp Leu Leu Asp Ser Ser			
	3540	3545	3550
Pro Val Phe Ala Ala Arg Ile Lys Glu Cys Ala Ala Ala Leu Glu Gln			
	3555	3560	3565
Trp Thr Asp Trp Ser Leu Leu Asp Val Leu Arg Gly Asp Ala Asp Leu			
	3570	3575	3580
Leu Asp Arg Val Asp Val Val Gln Pro Ala Ser Phe Ala Met Met Val			
3585	3590	3595	3600
Gly Leu Ala Ala Val Trp Thr Ser Leu Gly Val Thr Pro Asp Ala Val			
	3605	3610	3615
Leu Gly His Ser Gln Gly Glu Ile Ala Ala Ala Cys Val Ser Gly Ala			
	3620	3625	3630

Leu Ser Leu Asp Asp Ala Ala Lys Val Val Ala Leu Arg Ser Gln Ala
3635 3640 3645

Ile Ala Gly Glu Leu Ala Gly Arg Gly Gly Met Ala Ser Val Ala Leu
3650 3655 3660

Ser Glu Glu Asp Ala Val Ala Arg Leu Thr Pro Trp Ala Asn Arg Val
3665 3670 3675 3680

Glu Val Ala Ala Val Asn Ser Pro Ser Ser Val Val Ile Ala Gly Asp
3685 3690 3695

Ala Gln Ala Leu Asp Glu Ala Leu Glu Ala Leu Ala Gly Asp Gly Val
3700 3705 3710

Arg Val Arg Arg Val Ala Val Asp Tyr Ala Ser His Thr Arg His Val
3715 3720 3725

Glu Ala Ile Ala Glu Thr Leu Ala Lys Thr Leu Ala Gly Ile Asp Ala
3730 3735 3740

Arg Val Pro Ala Ile Pro Phe Tyr Ser Thr Val Leu Gly Thr Trp Ile
3745 3750 3755 3760

Glu Gln Ala Val Val Asp Ala Gly Tyr Trp Tyr Arg Asn Leu Arg Gln
3765 3770 3775

Gln Val Arg Phe Gly Pro Ser Val Ala Asp Leu Ala Gly Leu Gly His
3780 3785 3790

Thr Val Phe Val Glu Ile Ser Ala His Pro Val Leu Val Gln Pro Leu
3795 3800 3805

Ser Glu Ile Ser Asp Asp Ala Val Val Thr Gly Ser Leu Arg Arg Asp
3810 3815 3820

Asp Gly Gly Leu Arg Arg Leu Leu Ala Ser Ala Ala Glu Leu Tyr Val
3825 3830 3835 3840

Arg Gly Val Ala Val Asp Trp Thr Ala Ala Val Pro Ala Ala Gly Trp
3845 3850 3855

Val Asp Leu Pro Thr Tyr Ala Phe Asp Arg Arg His Phe Trp Leu His
3860 3865 3870

Glu Ala Glu Thr Ala Glu Ala Ala Glu Gly Met Asp Gly Glu Phe Trp
3875 3880 3885

Thr Ala Ile Glu Gln Ser Asp Val Asp Ser Leu Ala Glu Leu Leu Glu
3890 3895 3900

Leu Val Pro Glu Gln Arg Gly Ala Leu Ser Thr Val Val Pro Val Leu
3905 3910 3915 3920

Ala Gln Trp Arg Asp Arg Arg Arg Glu Arg Ser Thr Ala Glu Lys Leu
3925 3930 3935

Arg Tyr Gln Val Thr Trp Gln Pro Leu Glu Arg Glu Ala Ala Gly Val
3940 3945 3950

Pro Gly Gly Arg Trp Leu Ala Val Val Pro Ala Gly Thr Thr Asp Ala
3955 3960 3965

Leu Leu Lys Glu Leu Thr Gly Gln Gly Leu Asp Ile Val Arg Leu Glu
3970 3975 3980

Ile Glu Glu Ala Ser Arg Ala Gln Leu Ala Glu Gln Leu Arg Asn Val
3985 3990 3995 4000

Leu Ala Glu His Asp Leu Thr Gly Val Leu Ser Leu Leu Ala Leu Asp
4005 4010 4015

Gly Gly Pro Ala Asp Ala Ala Glu Ile Thr Ala Ser Thr Leu Ala Leu

4020	4025	4030
Val Gln Ala Leu Gly Asp Thr Thr Thr Ser Ala Pro Leu Trp Cys Leu		
4035	4040	4045
Thr Ser Gly Ala Val Asn Ile Gly Ile Gln Asp Ala Val Thr Ala Pro		
4050	4055	4060
Ala Gln Ala Ala Val Trp Gly Leu Gly Arg Ala Val Ala Leu Glu Arg		
4065	4070	4075 4080
Leu Asp Arg Trp Gly Gly Leu Val Asp Leu Pro Ala Ala Ile Asp Ala		
4085	4090	4095
Arg Thr Ala Gln Ala Leu Leu Gly Val Leu Asn Gly Ala Ala Gly Glu		
4100	4105	4110
Asp Gln Leu Ala Val Arg Arg Ser Gly Val Tyr Arg Arg Arg Leu Val		
4115	4120	4125
Arg Lys Pro Val Pro Glu Ser Ala Thr Ser Arg Trp Glu Pro Arg Gly		
4130	4135	4140
Thr Val Leu Val Thr Gly Gly Ala Glu Gly Leu Gly Arg His Ala Ser		
4145	4150	4155 4160
Val Trp Leu Ala Gln Ser Gly Ala Glu Arg Leu Ile Val Thr Gly Thr		
4165	4170	4175
Asp Gly Val Asp Glu Leu Thr Ala Glu Leu Ala Glu Phe Gly Thr Thr		
4180	4185	4190
Val Glu Phe Cys Ala Asp Thr Asp Arg Asp Ala Ile Ala Gln Leu Val		
4195	4200	4205
Ala Asp Ser Glu Val Thr Ala Val Val His Ala Ala Asp Ile Ala Gln		
4210	4215	4220

Thr Ser Ser Val Asp Asp Thr Gly Val Ala Asp Leu Asp Glu Val Phe
4225 4230 4235 4240

Ala Ala Lys Val Thr Thr Ala Val Trp Leu Asp Gln Leu Phe Glu Asp
4245 4250 4255

Thr Pro Leu Asp Ala Phe Val Val Phe Ser Ser Ile Ala Gly Ile Trp
4260 4265 4270

Gly Gly Gly Gly Gln Gly Pro Ala Gly Ala Ala Asn Ala Val Leu Asp
4275 4280 4285

Ala Leu Val Glu Trp Arg Arg Ala Arg Gly Leu Lys Ala Thr Ser Ile
4290 4295 4300

Ala Trp Gly Ala Leu Asp Gln Ile Gly Ile Gly Met Asp Glu Ala Ala
4305 4310 4315 4320

Leu Ala Gln Leu Arg Arg Arg Gly Val Ile Pro Met Ala Pro Pro Leu
4325 4330 4335

Ala Val Thr Ala Met Val Gln Ala Val Ala Gly Asn Glu Lys Ala Val
4340 4345 4350

Ala Val Ala Asp Met Asp Trp Ala Ala Phe Ile Pro Ala Phe Thr Ser
4355 4360 4365

Val Arg Pro Ser Pro Leu Phe Ala Asp Leu Pro Glu Ala Lys Ala Ile
4370 4375 4380

Leu Arg Ala Ala Gln Asp Asp Gly Glu Asp Gly Asp Thr Ala Ser Ser
4385 4390 4395 4400

Leu Ala Asp Ser Leu Arg Ala Val Pro Asp Ala Glu Gln Asn Arg Ile
4405 4410 4415

Leu Leu Lys Leu Val Arg Gly His Ala Ser Thr Val Leu Gly His Ser
4420 4425 4430

Gly Ala Glu Gly Ile Gly Pro Arg Gln Ala Phe Gln Glu Val Gly Phe
4435 4440 4445

Asp Ser Leu Ala Ala Val Asn Leu Arg Asn Ser Leu His Ala Ala Thr
4450 4455 4460

Gly Leu Arg Leu Pro Ala Thr Leu Ile Phe Asp Tyr Pro Thr Pro Glu
4465 4470 4475 4480

Ala Leu Val Gly Tyr Leu Arg Val Glu Leu Leu Arg Glu Ala Asp Asp
4485 4490 4495

Gly Leu Asp Gly Arg Glu Asp Asp Leu Arg Arg Val Leu Ala Ala Val
4500 4505 4510

Pro Phe Ala Arg Phe Lys Glu Ala Gly Val Leu Asp Thr Leu Leu Gly
4515 4520 4525

Leu Ala Asp Thr Gly Thr Glu Pro Gly Thr Asp Ala Glu Thr Thr Glu
4530 4535 4540

Ala Ala Pro Ala Ala Asp Asp Ala Glu Leu Ile Asp Ala Leu Asp Ile
4545 4550 4555 4560

Ser Gly Leu Val Gln Arg Ala Leu Gly Gln Thr Ser
4565 4570

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5069 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Met Ala Asn Gln Ser Trp Arg Lys Asn Met Ser Ala Pro Asn Glu Gln
1 5 10 15

Ile Val Asp Ala Leu Arg Ala Ser Leu Lys Glu Asn Val Arg Leu Gln
 20 25 30

Gln Glu Asn Ser Ala Leu Ala Ala Ala Ala Glu Pro Val Ala Ile
 35 40 45

Val Ser Met Ala Cys Arg Tyr Ala Gly Gly Ile Arg Gly Pro Glu Asp
 50 55 60

Phe Trp Arg Val Val Ser Glu Gly Ala Asp Val Tyr Thr Gly Phe Pro
65 70 75 80

Glu Asp Arg Gly Trp Asp Val Glu Gly Leu Tyr His Pro Asp Pro Asp
 85 90 95

Asn Pro Gly Thr Thr Tyr Val Arg Glu Gly Ala Phe Leu Gln Asp Ala
 100 105 110

Ala Gln Phe Asp Ala Gly Phe Phe Gly Ile Ser Pro Arg Glu Ala Leu
 115 120 125

Ala Met Asp Pro Gln Gln Arg Gln Leu Leu Glu Val Ser Trp Glu Thr
 130 135 140

Leu Glu Arg Ala Gly Ile Asp Pro His Ser Val Arg Gly Ser Asp Ile
145 150 155 160

Gly Val Tyr Ala Gly Val Val His Gln Asp Tyr Ala Pro Asp Leu Ser
165 170 175

Gly Phe Glu Gly Phe Met Ser Leu Glu Arg Ala Leu Gly Thr Ala Gly
180 185 190

Gly Val Ala Ser Gly Arg Val Ala Tyr Thr Leu Gly Leu Glu Gly Pro
195 200 205

Ala Val Thr Val Asp Thr Met Cys Ser Ser Ser Leu Val Ala Ile His
210 215 220

Leu Ala Ala Gln Ala Leu Arg Arg Gly Glu Cys Ser Met Ala Leu Ala
225 230 235 240

Gly Gly Ser Thr Val Met Ala Thr Pro Gly Gly Phe Val Gly Phe Ala
245 250 255

Arg Gln Arg Ala Leu Ala Phe Asp Gly Arg Cys Lys Ser Tyr Ala Ala
260 265 270

Ala Ala Asp Gly Ser Gly Trp Ala Glu Gly Val Gly Val Leu Leu Leu
275 280 285

Glu Arg Leu Ser Val Ala Arg Glu Arg Gly His Gln Val Leu Ala Val
290 295 300

Ile Arg Gly Ser Ala Val Asn Gln Asp Gly Ala Ser Asn Gly Leu Thr
305 310 315 320

Ala Pro Asn Gly Pro Ala Gln Gln Arg Val Ile Arg Lys Ala Leu Ala
325 330 335

Ser Ala Gly Leu Thr Pro Ser Asp Val Asp Thr Val Glu Gly His Gly
340 345 350

20603"532404

Thr Gly Thr Val Leu Gly Asp Pro Ile Glu Val Gln Ala Leu Leu Ala
355 360 365

Thr Tyr Gly Gln Gly Arg Asp Pro Gln Gln Pro Leu Trp Leu Gly Ser
370 375 380

Val Lys Ser Val Val Gly His Thr Gln Ala Ala Ser Gly Val Ala Gly
385 390 395 400

Val Ile Lys Met Val Gln Ser Leu Arg His Gly Gln Leu Pro Ala Thr
405 410 415

Gln His Val Asp Ala Pro Thr Pro Gln Val Asp Trp Ser Ala Gly Ala
420 425 430

Ile Glu Leu Leu Ala Glu Gly Arg Glu Trp Pro Arg Asn Gly His Pro
435 440 445

Arg Arg Gly Gly Ile Ser Ser Phe Gly Ala Ser Gly Thr Asn Ala His
450 455 460

Met Ile Leu Glu Glu Ala Pro Glu Asp Glu Pro Val Thr Glu Ala Pro
465 470 475 480

Ala Pro Thr Gly Val Val Pro Leu Val Val Ser Ala Ala Thr Ala Ala
485 490 495

Ser Leu Ala Ala Gln Ala Gly Arg Leu Ala Glu Val Gly Asp Val Ser
500 505 510

Leu Ala Asp Val Ala Gly Thr Leu Val Ser Gly Arg Ala Met Leu Ser
515 520 525

Glu Arg Ala Val Val Val Ala Gly Ser His Glu Glu Ala Val Thr Gly
530 535 540

Leu Arg Ala Leu Ala Arg Gly Glu Ser Ala Pro Gly Leu Leu Ser Gly

545	550	555	560
Arg Gly Ser Gly Val Pro Gly Lys Val Val Trp Val Phe Pro Gly Gln			
565	570	575	
Gly Thr Gln Trp Ala Gly Met Gly Arg Glu Leu Leu Asp Ser Ser Glu			
580	585	590	
Val Phe Ala Ala Arg Ile Ala Glu Cys Glu Thr Ala Leu Gly Arg Trp			
595	600	605	
Val Asp Trp Ser Leu Thr Asp Val Leu Arg Gly Glu Ala Asp Leu Leu			
610	615	620	
Asp Arg Val Asp Val Val Gln Pro Ala Ser Phe Ala Val Met Val Gly			
625	630	635	640
Leu Ala Ala Val Trp Ala Ser Leu Gly Val Glu Pro Glu Ala Val Val			
645	650	655	
Gly His Ser Gln Gly Glu Ile Ala Ala Ala Cys Val Ser Gly Ala Leu			
660	665	670	
Ser Leu Glu Asp Ala Ala Lys Val Val Ala Leu Arg Ser Gln Ala Ile			
675	680	685	
Ala Ala Ser Leu Ala Gly Arg Gly Gly Met Ala Ser Val Ala Leu Ser			
690	695	700	
Glu Glu Asp Ala Thr Ala Arg Leu Glu Pro Trp Ala Gly Arg Val Glu			
705	710	715	720
Val Ala Ala Val Asn Gly Pro Thr Ser Val Val Ile Ala Gly Asp Ala			
725	730	735	
Glu Ala Leu Asp Glu Ala Leu Asp Ala Leu Asp Asp Gln Gly Val Arg			
740	745	750	

Gly Ala Asp His Pro Leu Leu Gly Ala Val Val Pro Leu Pro Gln Ser
930 935 940

Asp Gly Leu Val Phe Thr Ser Arg Leu Ser Leu Lys Ser His Pro Trp
945 950 955 960

Leu Ala Gly His Ala Ile Gly Gly Val Val Leu Ile Pro Gly Thr Val
965 970 975

Tyr Val Asp Leu Ala Leu Arg Ala Gly Asp Glu Leu Gly Phe Gly Val
980 985 990

Leu Glu Glu Leu Val Ile Glu Ala Pro Leu Val Leu Gly Glu Arg Gly
995 1000 1005

Gly Val Arg Val Gln Val Ala Val Ser Gly Pro Asn Glu Thr Gly Ser
1010 1015 1020

Arg Ala Val Asp Val Phe Ser Met Arg Glu Asp Gly Asp Glu Trp Thr
1025 1030 1035 1040

Arg His Ala Thr Gly Leu Leu Gly Ala Ser Thr Ser Arg Glu Pro Ser
1045 1050 1055

Arg Phe Asp Phe Ala Ala Trp Pro Pro Ala Gly Ala Glu Pro Ile Asp
1060 1065 1070

Val Glu Asn Phe Tyr Thr Asp Leu Thr Glu Arg Gly Tyr Ala Tyr Ser
1075 1080 1085

Gly Ala Phe Gln Gly Met Arg Ala Val Trp Arg Arg Gly Asp Glu Val
1090 1095 1100

Phe Ala Glu Val Ala Leu Pro Asp Asp His Arg Glu Asp Ala Gly Lys
1105 1110 1115 1120

Phe Gly Leu His Pro Ala Leu Leu Asp Ala Ala Leu His Thr Asn Ala
1125 1130 1135

Phe Ala Asn Pro Asp Asp Asp Arg Ser Val Leu Pro Phe Ala Trp Asn

1140	1145	1150
Gly Leu Val Leu His Ala Val Gly Ala Ser Ala Leu Arg Val Arg Val		
1155	1160	1165
Ala Pro Gly Gly Pro Asp Ala Leu Thr Phe Gln Ala Ala Asp Glu Thr		
1170	1175	1180
Gly Gly Leu Val Val Thr Met Asp Ser Leu Val Ser Arg Glu Val Ser		
1185	1190	1195 1200
Ala Ala Gln Leu Glu Thr Ala Ala Gly Glu Glu Arg Asp Ser Leu Phe		
1205	1210	1215
Gln Val Asp Trp Ile Glu Val Pro Ala Thr Glu Thr Ala Ala Thr Glu		
1220	1225	1230
His Ala Glu Val Leu Glu Ala Phe Gly Glu Ala Ala Pro Leu Glu Leu		
1235	1240	1245
Thr Ser Arg Val Leu Glu Ala Val Gln Ser Trp Leu Ala Asp Ala Ala		
1250	1255	1260
Asp Glu Ala Arg Leu Val Val Val Thr Arg Gly Ala Val Arg Glu Val		
1265	1270	1275 1280
Thr Asp Pro Ala Gly Ala Ala Val Trp Gly Leu Val Arg Ala Ala Gln		
1285	1290	1295
Ala Glu Asn Pro Gly Arg Ile Ile Leu Val Asp Thr Asp Gly Asp Val		
1300	1305	1310
Pro Leu Gly Ala Val Leu Ala Ser Gly Glu Pro Gln Leu Ala Val Arg		
1315	1320	1325
Gly Asn Ala Phe Ser Val Pro Arg Leu Ala Arg Ala Thr Gly Glu Val		
1330	1335	1340

Pro Glu Ala Pro Ala Val Phe Ser Pro Glu Gly Thr Val Leu Leu Thr
1345 1350 1355 1360

Gly Gly Thr Gly Ser Leu Gly Gly Leu Val Ala Lys His Leu Val Ala
1365 1370 1375

Arg His Gly Val Arg Arg Leu Val Leu Ala Ser Arg Arg Gly Val Ala
1380 1385 1390

Ala Glu Asp Leu Val Thr Glu Leu Thr Glu Gln Gly Ala Thr Val Ser
1395 1400 1405

Val Val Ala Cys Asp Val Ser Asp Arg Asp Gln Val Ala Ala Leu Leu
1410 1415 1420

Ala Glu His Arg Pro Thr Gly Ile Val His Leu Ala Gly Leu Leu Asp
1425 1430 1435 1440

Asp Gly Val Ile Gly Ala Leu Asn Arg Glu Arg Leu Ala Gly Val Phe
1445 1450 1455

Ala Pro Lys Val Asp Ala Val Gln His Leu Asp Glu Leu Thr Arg Asp
1460 1465 1470

Leu Gly Leu Asp Ala Phe Val Val Phe Ser Ser Ala Ala Ala Leu Met
1475 1480 1485

Gly Ser Ala Gly Gln Gly Asn Tyr Ala Ala Ala Asn Ala Phe Leu Asp
1490 1495 1500

Gly Leu Met Ala Gly Arg Arg Ala Ala Gly Leu Pro Gly Val Ser Leu
1505 1510 1515 1520

Ala Trp Gly Leu Trp Glu Gln Ala Asp Gly Leu Thr Ala Asn Leu Ser
1525 1530 1535

Ala Thr Asp Gln Ala Arg Met Ser Arg Gly Gly Val Leu Pro Met Thr
1540 1545 1550

Pro Ala Glu Ala Leu Asp Ile Phe Asp Ile Gly Leu Ala Ala Glu Gln
1555 1560 1565

Ala Leu Leu Val Pro Ile Lys Leu Asp Leu Arg Thr Leu Arg Gly Gln
1570 1575 1580

Ala Thr Ala Gly Gly Glu Val Pro His Leu Leu Arg Gly Leu Val Arg
1585 1590 1595 1600

Ala Ser Arg Arg Val Thr Arg Thr Ala Ala Ala Ser Gly Gly Gly Gly
1605 1610 1615

Leu Val His Lys Leu Ala Gly Arg Pro Ala Glu Glu Gln Glu Ala Val
1620 1625 1630

Leu Leu Gly Ile Val Gln Ala Glu Ala Ala Ala Val Leu Gly Phe Asn
1635 1640 1645

Ala Pro Glu Leu Ala Gln Gly Thr Arg Gly Phe Ser Asp Leu Gly Phe
1650 1655 1660

Asp Ser Leu Thr Ala Val Glu Leu Arg Asn Arg Leu Ser Ala Ala Thr
1665 1670 1675 1680

Gly Val Lys Leu Pro Ala Thr Leu Val Phe Asp Tyr Pro Thr Pro Val
1685 1690 1695

Ala Leu Ala Arg His Leu Arg Glu Glu Leu Gly Glu Thr Val Ala Gly
1700 1705 1710

Ala Pro Ala Thr Pro Val Thr Thr Val Ala Asp Ala Gly Glu Pro Ile
1715 1720 1725

Ala Ile Val Gly Met Ala Cys Arg Leu Pro Gly Gly Val Met Ser Pro

1730	1735	1740	
Asp Asp Leu Trp Arg Met Val Ala Glu Gly Arg Asp Gly Met Ser Pro			
1745	1750	1755	1760
Phe Pro Gly Asp Arg Gly Trp Asp Leu Asp Gly Leu Phe Asp Ser Asp			
	1765	1770	1775
Pro Glu Arg Pro Gly Thr Ala Tyr Ile Arg Gln Gly Gly Phe Leu His			
	1780	1785	1790
Glu Ala Ala Leu Phe Asp Pro Gly Phe Phe Gly Ile Ser Pro Arg Glu			
	1795	1800	1805
Ala Leu Ala Met Asp Pro Gln Gln Arg Leu Leu Leu Glu Ala Ser Trp			
	1810	1815	1820
Glu Ala Leu Glu Arg Ala Gly Ile Asp Pro Thr Lys Ala Arg Gly Asp			
1825	1830	1835	1840
Ala Val Gly Val Phe Ser Gly Val Ser Ile His Asp Tyr Leu Glu Ser			
	1845	1850	1855
Leu Ser Asn Met Pro Ala Glu Leu Glu Gly Phe Val Thr Thr Ala Thr			
	1860	1865	1870
Ala Gly Ser Val Ala Ser Gly Arg Val Ser Tyr Thr Phe Gly Phe Glu			
	1875	1880	1885
Gly Pro Ala Val Thr Val Asp Thr Ala Cys Ser Ser Ser Leu Val Ala			
	1890	1895	1900
Ile His Leu Ala Ala Gln Ala Leu Arg Gln Gly Glu Cys Thr Met Ala			
1905	1910	1915	1920
Leu Ala Gly Gly Val Ala Val Met Gly Ser Pro Ile Gly Val Ile Gly			
	1925	1930	1935

1936 1937 1938 1939 1940 1941 1942 1943 1944 1945 1946 1947 1948 1949 1950 1951 1952 1953 1954 1955 1956 1957 1958 1959 1960 1961 1962 1963 1964 1965 1966 1967 1968 1969 1970 1971 1972 1973 1974 1975 1976 1977 1978 1979 1980 1981 1982 1983 1984 1985 1986 1987 1988 1989 1990 1991 1992 1993 1994 1995 1996 1997 1998 1999 2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613 2614 2615 2616 2617 2618 2619 2620 2621 2622 2623 2624 2625 2626 2627 2628 2629 2630 2631 2632 2633 2634 2635 2636 2637 2638 2639 2640 2641 2642 2643 2644 2645 2646 2647 2648 2649 2650 2651 2652 2653 2654 2655 2656 2657 2658 2659 2660 2661 2662 2663 2664 2665 2666 2667 2668 2669 2670 2671 2672 2673 2674 2675 2676 2677 2678 2679 2680 2681 2682 2683 2684 2685 2686 2687 2688 2689 2690 2691 2692 2693 2694 2695 2696 2697 2698 2699 2700 2701 2702 2703 2704 2705 2706 2707 2708 2709 2710 2711 2712 2713 2714 2715 2716 2717 2718 2719 2720 2721 2722 2723 2724 2725 2726 2727 2728 2729 2730 2731 2732 2733 2734 2735 2736 2737 2738 2739 2740 2741 2742 2743 2744 2745 2746 2747 2748 2749 2750 2751 2752 2753 2754 2755 2756 2757 2758 2759 2760 2761 2762 2763 2764 2765 2766 2767 2768 2769 2770 2771 2772 2773 2774 2775 2776 2777 2778 2779 2780 2781 2782 2783 2784 2785 2786 2787 2788 2789 2790 2791 2792 2793 2794 2795 2796 2797 2798 2799 2800 2801 2802 2803 2804 2805 2806 2807 2808 2809 2810 2811 2812 2813 2814 2815 2816 2817 2818 2819 2820 2821 2822 2823 2824 2825 2826 2827 2828 2829 2830 2831 2832 2833 2834 2835 2836 2837 2838 2839 2840 2841 2842 2843 2844 2845 2846 2847 2848 2849 2850 2851 2852 2853 2854 2855 2856 2857 2858 2859 2860 2861 2862 2863 2864 2865 2866 2867 2868 2869 2870 2871 2872 2873 2874 2875 2876 2877 2878 2879 2880 2881 2882 2883 2884 2885 2886 2887 2888 2889 2890 2891 2892 2893 2894 2895 2896 2897 2898 2899 2900 2901 2902 2903 2904 2905 2906 2907 2908 2909 2910 2911 2912 2913 2914 2915 2916 2917 2918 2919 2920 2921 2922 2923 2924 2925 2926 2927 2928 2929 2930 2931 2932 2933 2934 2935 2936 2937 2938 2939 2940 2941 2942 2943 2944 2945 2946 2947 2948 2949 2950 2951 2952 2953 2954 2955 2956 2957 2958 2959 2960 2961 2962 2963 2964 2965 2966 2967 2968 2969 2970 2971 2972 2973 2974 2975 2976 2977 2978 2979 2980 2981 2982 2983 2984 2985 2986 2987 2988 2989 2990 2991 2992 2993 2994 2995 2996 2997 2998 2999 3000

Met Ser Arg Gln Arg Gly Met Ala Glu Asp Gly Arg Val Lys Ala Phe
1940 1945 1950

Ala Asp Gly Ala Asp Gly Thr Val Leu Ser Glu Gly Val Gly Ile Val
1955 1960 1965

Val Leu Glu Arg Leu Ser Val Ala Arg Glu Arg Gly His Arg Val Leu
1970 1975 1980

Ala Val Leu Arg Gly Ser Ala Val Asn Gln Asp Gly Ala Ser Asn Gly
1985 1990 1995 2000

Leu Thr Ala Pro Asn Gly Pro Ser Gln Gln Arg Val Ile Arg Ser Ala
2005 2010 2015

Leu Ala Gly Ala Gly Leu Gln Pro Ser Glu Val Asp Val Val Glu Ala
2020 2025 2030

His Gly Thr Gly Thr Ala Leu Gly Glu Pro Ile Glu Ala Gln Ala Leu
2035 2040 2045

Leu Ala Thr Tyr Gly Lys Ser Arg Glu Thr Pro Leu Trp Leu Gly Ser
2050 2055 2060

Leu Lys Ser Asn Ile Gly His Thr Gln Ala Ala Ala Gly Val Ala Ala
2065 2070 2075 2080

Val Ile Lys Met Val Gln Ala Leu Arg Gln Asp Thr Leu Pro Pro Thr
2085 2090 2095

Leu His Val Gln Glu Pro Thr Lys Gln Val Asp Trp Ser Ala Gly Ala
2100 2105 2110

Val Glu Leu Leu Thr Glu Gly Arg Glu Trp Ala Arg Asn Gly His Pro
2115 2120 2125

Arg Arg Ala Gly Val Ser Ser Phe Gly Ile Ser Gly Thr Asn Ala His
2130 2135 2140

Leu Ile Leu Glu Glu Ala Pro Ala Asp Asp Thr Ala Glu Ala Asp Val
2145 2150 2155 2160

Pro Asp Ala Val Val Pro Val Val Ile Ser Ala Arg Ser Thr Gly Ser
2165 2170 2175

Leu Ala Gly Gln Ala Gly Arg Leu Ala Ala Phe Leu Asp Gly Asp Val
2180 2185 2190

Pro Leu Thr Arg Val Ala Gly Ala Leu Leu Ser Thr Arg Ala Thr Leu
2195 2200 2205

Thr Asp Arg Ala Val Val Val Ala Gly Ser Ala Glu Glu Ala Arg Ala
2210 2215 2220

Gly Leu Thr Ala Leu Ala Arg Gly Glu Ser Ala Ser Gly Leu Val Thr
2225 2230 2235 2240

Gly Thr Ala Gly Met Pro Gly Lys Thr Val Trp Val Phe Pro Gly Gln
2245 2250 2255

Gly Thr Gln Trp Ala Gly Met Gly Arg Glu Leu Leu Glu Ala Ser Pro
2260 2265 2270

Val Phe Ala Glu Arg Ile Glu Glu Cys Ala Ala Ala Leu Gln Pro Trp
2275 2280 2285

Ile Asp Trp Ser Leu Leu Asp Val Leu Arg Gly Glu Gly Glu Leu Asp
2290 2295 2300

Arg Val Asp Val Leu Gln Pro Ala Cys Phe Ala Val Met Val Gly Leu
2305 2310 2315 2320

Ala Ala Val Trp Ala Ser Val Gly Val Val Pro Asp Ala Val Leu Gly

2335

2350

2365

2380

2400

2415

2430

2445

2460

2480

2495

2510

2525

Val Val Thr Gly Thr Leu Arg Arg Asp Asp Gly Gly Val Arg Arg Leu
2530 2535 2540

Leu Thr Ser Met Ala Glu Leu Phe Val Arg Gly Val Pro Val Asp Trp
2545 2550 2555 2560

Ala Thr Met Ala Pro Pro Ala Arg Val Glu Leu Pro Thr Tyr Ala Phe
2565 2570 2575

Asp His Gln His Phe Trp Leu Ser Pro Pro Ala Val Ala Asp Ala Pro
2580 2585 2590

Ala Leu Gly Leu Ala Gly Ala Asp His Pro Leu Leu Gly Ala Val Leu
2595 2600 2605

Pro Leu Pro Gln Ser Asp Gly Leu Val Phe Thr Ser Arg Leu Ser Val
2610 2615 2620

Arg Thr His Pro Trp Leu Ala Asp Gly Val Pro Ala Ala Ala Leu Val
2625 2630 2635 2640

Glu Leu Ala Val Arg Ala Gly Asp Glu Ala Gly Cys Pro Val Leu Ala
2645 2650 2655

Asp Leu Thr Val Glu Lys Leu Leu Val Leu Pro Glu Ser Gly Gly Leu
2660 2665 2670

Arg Val Gln Val Ile Val Ser Gly Glu Arg Thr Val Glu Val Tyr Ser
2675 2680 2685

Gln Leu Glu Gly Ala Glu Asp Trp Ile Arg Asn Ala Thr Gly His Leu
2690 2695 2700

Ser Ala Thr Ala Pro Ala His Glu Ala Phe Asp Phe Thr Ala Trp Pro
2705 2710 2715 2720

Pro Ala Gly Ala Gln Gln Val Asp Gly Leu Trp Arg Arg Gly Asp Glu
2725 2730 2735

Ile Phe Ala Glu Val Ala Leu Pro Glu Glu Leu Asp Ala Gly Ala Phe
2740 2745 2750

Gly Ile His Pro Phe Leu Leu Asp Ala Ala Val Gln Pro Val Leu Ala
2755 2760 2765

Asp Asp Glu Gln Pro Ala Glu Trp Arg Ser Leu Val Leu His Ala Ala
2770 2775 2780

Gly Ala Ser Ala Leu Arg Val Arg Leu Val Pro Gly Gly Ala Leu Gln
2785 2790 2795 2800

Ala Ala Asp Glu Thr Gly Gly Leu Val Leu Thr Ala Asp Ser Val Ala
2805 2810 2815

Gly Arg Glu Leu Ser Ala Gly Lys Thr Arg Ala Gly Ser Leu Tyr Arg
2820 2825 2830

Val Asp Trp Thr Glu Val Ser Ile Ala Asp Ser Ala Val Pro Ala Asn
2835 2840 2845

Ile Glu Val Val Glu Ala Phe Gly Glu Glu Pro Leu Glu Leu Thr Gly
2850 2855 2860

Arg Val Leu Glu Ala Val Gln Thr Trp Leu Val Thr Ala Ala Asp Asp
2865 2870 2875 2880

Ala Arg Leu Val Val Val Thr Arg Gly Ala Val Arg Glu Val Thr Asp
2885 2890 2895

Pro Ala Gly Ala Ala Val Trp Gly Leu Val Arg Ala Ala Gln Ala Glu
2900 2905 2910

Asn Pro Gly Arg Ile Phe Leu Ile Asp Thr Asp Gly Glu Ile Pro Ala

20250101 10:00:00

2915	2920	2925
Leu Thr Gly Asp Glu Pro Glu Ile Ala Val Arg Gly Gly Lys Phe Phe		
2930	2935	2940
Val Pro Arg Ile Thr Arg Ala Glu Pro Ser Gly Ala Ala Val Phe Arg		
2945	2950	2955 2960
Pro Asp Gly Thr Val Leu Ile Ser Gly Ala Gly Ala Leu Gly Gly Leu		
2965	2970	2975
Val Ala Arg Arg Leu Val Glu Arg His Gly Val Arg Lys Leu Val Leu		
2980	2985	2990
Ala Ser Arg Arg Gly Arg Asp Ala Asp Gly Val Ala Asp Leu Val Ala		
2995	3000	3005
Asp Leu Ala Ala Asp Val Ser Val Val Ala Cys Asp Val Ser Asp Arg		
3010	3015	3020
Ala Gln Val Ala Ala Leu Leu Asp Glu His Arg Pro Thr Ala Val Val		
3025	3030	3035 3040
His Thr Ala Gly Val Ile Asp Ala Gly Val Ile Glu Thr Leu Asp Arg		
3045	3050	3055
Asp Arg Leu Ala Thr Val Phe Ala Pro Lys Val Asp Ala Val Arg His		
3060	3065	3070
Leu Asp Glu Leu Thr Arg Asp Arg Asp Leu Asp Ala Phe Val Val Tyr		
3075	3080	3085
Ser Ser Val Ser Ala Val Phe Met Gly Ala Gly Ser Gly Ser Tyr Ala		
3090	3095	3100
Ala Ala Asn Ala Phe Leu Asp Gly Leu Met Ala Asn Arg Arg Ala Ala		
3105	3110	3115 3120

Gly Leu Pro Gly Leu Ser Leu Ala Trp Gly Leu Trp Asp Gln Ser Thr
3125 3130 3135

Gly Met Ala Ala Gly Thr Asp Glu Ala Thr Arg Ala Arg Met Ser Arg
3140 3145 3150

Arg Gly Gly Leu Gln Ile Met Thr Gln Ala Glu Gly Met Asp Leu Phe
3155 3160 3165

Asp Ala Ala Leu Ser Ser Ala Glu Ser Leu Leu Val Pro Ala Lys Leu
3170 3175 3180

Asp Leu Arg Gly Val Arg Ala Asp Ala Ala Ala Gly Gly Val Val Pro
3185 3190 3195 3200

His Met Leu Arg Gly Leu Val Arg Ala Gly Arg Ala Gln Ala Arg Ala
3205 3210 3215

Ala Ser Thr Val Asp Asn Gly Leu Ala Gly Arg Leu Ala Gly Leu Ala
3220 3225 3230

Pro Ala Asp Gln Leu Thr Leu Leu Leu Asp Leu Val Arg Ala Gln Val
3235 3240 3245

Ala Ala Val Leu Gly His Ala Asp Ala Ser Ala Val Arg Val Asp Thr
3250 3255 3260

Ala Phe Lys Asp Ala Gly Phe Asp Ser Leu Thr Ala Val Glu Leu Arg
3265 3270 3275 3280

Asn Arg Met Arg Thr Ala Thr Gly Leu Lys Leu Pro Ala Thr Leu Val
3285 3290 3295

Phe Asp Tyr Pro Asn Pro Gln Ala Leu Ala Arg His Leu Arg Asp Glu
3300 3305 3310

Leu Gly Gly Ala Ala Gln Thr Pro Val Thr Thr Ala Ala Ala Lys Ala
3315 3320 3325

Asp Leu Asp Glu Pro Ile Ala Ile Val Gly Met Ala Cys Arg Leu Pro
3330 3335 3340

Gly Gly Val Ala Gly Pro Glu Asp Leu Trp Arg Leu Val Ala Glu Gly
3345 3350 3355 3360

Arg Asp Ala Val Ser Ser Phe Pro Thr Asp Arg Gly Trp Asp Thr Asp
3365 3370 3375

Ser Leu Tyr Asp Pro Asp Pro Ala Arg Pro Gly Lys Thr Tyr Thr Arg
3380 3385 3390

His Gly Gly Phe Leu His Glu Ala Gly Leu Phe Asp Ala Gly Phe Phe
3395 3400 3405

Gly Ile Ser Pro Arg Glu Ala Val Ala Met Asp Pro Gln Gln Arg Leu
3410 3415 3420

Leu Leu Glu Ala Ser Trp Glu Ala Met Glu Asp Ala Gly Val Asp Pro
3425 3430 3435 3440

Leu Ser Leu Lys Gly Asn Asp Val Gly Val Phe Thr Gly Met Phe Gly
3445 3450 3455

Gln Gly Tyr Val Ala Pro Gly Asp Ser Val Val Thr Pro Glu Leu Glu
3460 3465 3470

Gly Phe Ala Gly Thr Gly Gly Ser Ser Ser Val Ala Ser Gly Arg Val
3475 3480 3485

Ser Tyr Val Phe Gly Phe Glu Gly Pro Ala Val Thr Ile Asp Ser Ala
3490 3495 3500

Cys Ser Ser Ser Leu Val Ala Met His Leu Ala Ala Gln Ser Leu Arg

3505	3510	3515	3520
Gln Gly Glu Cys Ser Met Ala Leu Ala Gly Gly Ala Thr Val Met Ala			
	3525	3530	3535
Asn Pro Gly Ala Phe Val Glu Phe Ser Arg Gln Arg Gly Leu Ala Val			
	3540	3545	3550
Asp Gly Arg Cys Lys Ala Phe Ala Ala Ala Asp Gly Thr Gly Trp			
	3555	3560	3565
Ala Glu Gly Val Gly Val Val Ile Leu Glu Arg Leu Ser Val Ala Arg			
	3570	3575	3580
Glu Arg Gly His Arg Ile Leu Ala Val Leu Arg Gly Ser Ala Val Asn			
3585	3590	3595	3600
Gln Asp Gly Ala Ser Asn Gly Leu Thr Ala Pro Asn Gly Pro Ser Gln			
	3605	3610	3615
Gln Arg Val Ile Arg Arg Ala Leu Val Ser Ala Gly Leu Ala Pro Ser			
	3620	3625	3630
Asp Val Asp Val Val Glu Ala His Gly Thr Gly Thr Thr Leu Gly Asp			
	3635	3640	3645
Pro Ile Glu Ala Gln Ala Leu Leu Ala Thr Tyr Gly Lys Asp Arg Glu			
3650	3655	3660	
Ser Pro Leu Trp Leu Gly Ser Leu Lys Ser Asn Ile Gly His Ala Gln			
3665	3670	3675	3680
Ala Ala Ala Gly Val Ala Gly Val Ile Lys Met Val Gln Ala Leu Arg			
	3685	3690	3695
His Glu Val Leu Pro Pro Thr Leu His Val Asp Arg Pro Thr Pro Glu			
	3700	3705	3710

Val Asp Trp Ser Ala Gly Ala Val Glu Leu Leu Thr Glu Ala Arg Glu
3715 3720 3725

Trp Pro Arg Asn Gly Arg Pro Arg Arg Ala Gly Val Ser Ala Phe Gly
3730 3735 3740

Val Ser Gly Thr Asn Ala His Leu Ile Leu Glu Glu Ala Pro Ala Glu
3745 3750 3755 3760

Glu Pro Val Pro Thr Pro Glu Val Pro Leu Val Pro Val Val Val Ser
3765 3770 3775

Ala Arg Ser Arg Ala Ser Leu Ala Gly Gln Ala Gly Arg Leu Ala Gly
3780 3785 3790

Phe Val Ala Gly Asp Ala Ser Leu Ala Gly Val Ala Arg Ala Leu Val
3795 3800 3805

Thr Asn Arg Ala Ala Leu Thr Glu Arg Ala Val Met Val Val Gly Ser
3810 3815 3820

Arg Glu Glu Ala Val Thr Asn Leu Glu Ala Leu Ala Arg Gly Glu Asp
3825 3830 3835 3840

Pro Ala Ala Val Val Thr Gly Arg Ala Gly Ser Pro Gly Lys Leu Val
3845 3850 3855

Trp Val Phe Pro Gly Gln Gly Ser Gln Trp Ile Gly Met Gly Arg Glu
3860 3865 3870

Leu Leu Asp Ser Ser Pro Val Phe Ala Glu Arg Val Ala Glu Cys Ala
3875 3890 3885

Ala Ala Leu Glu Pro Trp Ile Asp Trp Ser Leu Leu Asp Val Leu Arg
3890 3895 3900

Gly Glu Ser Asp Leu Leu Asp Arg Val Asp Val Val Gln Pro Ala Ser
3905 3910 3915 3920

Phe Ala Met Met Val Gly Leu Ala Ala Val Trp Gln Ser Val Gly Val
3925 3930 3935

Arg Pro Asp Ala Val Val Gly His Ser Gln Gly Glu Ile Ala Ala Ala
3940 3945 3950

Cys Val Ser Gly Ala Leu Ser Leu Gln Asp Ala Ala Lys Val Val Ala
3955 3960 3965

Leu Arg Ser Gln Ala Ile Ala Thr Arg Leu Ala Gly Arg Gly Gly Met
3970 3975 3980

Ala Ser Val Ala Leu Ser Glu Glu Asp Ala Thr Ala Trp Leu Ala Pro
3985 3990 3995 4000

Trp Ala Asp Arg Val Gln Val Ala Ala Val Asn Ser Pro Ala Ser Val
4005 4010 4015

Val Ile Ala Gly Glu Ala Gln Ala Leu Asp Glu Val Val Asp Ala Leu
4020 4025 4030

Ser Gly Gln Glu Val Arg Val Arg Arg Val Ala Val Asp Tyr Gly Ser
4035 4040 4045

His Thr Asn Gln Val Glu Ala Ile Glu Asp Leu Leu Ala Glu Thr Leu
4050 4055 4060

Ala Gly Ile Glu Ala Gln Ala Pro Lys Val Pro Phe Tyr Ser Thr Leu
4065 4070 4075 4080

Ile Gly Asp Trp Ile Arg Asp Ala Gly Ile Val Asp Gly Gly Tyr Trp
4085 4090 4095

Tyr Arg Asn Leu Arg Asn Gln Val Gly Phe Gly Pro Ala Val Ala Glu

3905 3910 3915 3920 3925 3930 3935 3940 3945 3950 3955 3960 3965 3970 3975 3980 3985 3990 3995 4000 4005 4010 4015 4020 4025 4030 4035 4040 4045 4050 4055 4060 4065 4070 4075 4080 4085 4090 4095

4100	4105	4110
Leu Val Arg Gln Gly His Gly Val Phe Val Glu Val Ser Ala His Pro		
4115	4120	4125
Val Leu Val Gln Pro Leu Ser Glu Leu Ser Asp Asp Ala Val Val Thr		
4130	4135	4140
Gly Ser Leu Arg Arg Glu Asp Gly Gly Leu Arg Arg Leu Leu Thr Ser		
4145	4150	4155 4160
Met Ala Glu Leu Tyr Val Gln Gly Val Pro Leu Asp Trp Thr Ala Val		
4165	4170	4175
Leu Pro Arg Thr Gly Arg Val Asp Leu Pro Lys Tyr Ala Phe Asp His		
4180	4185	4190
Arg His Tyr Trp Leu Arg Pro Ala Glu Ser Ala Thr Asp Ala Ala Ser		
4195	4200	4205
Leu Gly Gln Ala Ala Ala Asp His Pro Leu Leu Gly Ala Val Val Glu		
4210	4215	4220
Leu Pro Gln Ser Asp Gly Leu Val Phe Thr Ser Arg Leu Ser Val Arg		
4225	4230	4235 4240
Thr His Pro Trp Leu Ala Asp His Ala Val Gly Gly Val Val Ile Leu		
4245	4250	4255
Pro Gly Ser Gly Leu Ala Glu Leu Ala Val Arg Ala Gly Asp Glu Ala		
4260	4265	4270
Gly Cys Thr Ala Leu Asp Glu Leu Ile Ile Glu Ala Pro Leu Val Val		
4275	4280	4285
Pro Ala Gln Gly Ala Val Arg Val Gln Val Ala Leu Ser Gly Pro Asp		
4290	4295	4300

Glu Thr Gly Ser Arg Thr Val Asp Leu Tyr Ser Gln Arg Asp Gly Gly
4305 4310 4315 4320

Ala Gly Thr Trp Thr Arg His Ala Thr Gly Val Leu Ser Thr Ala Pro
4325 4330 4335

Ala Gln Glu Pro Glu Phe Asp Phe His Ala Trp Pro Pro Ala Asp Ala
4340 4345 4350

Glu Arg Ile Asp Val Glu Thr Phe Tyr Thr Asp Leu Ala Glu Arg Gly
4355 4360 4365

Tyr Gly Tyr Gly Pro Ala Phe Gln Gly Leu Gln Ala Val Trp Arg Arg
4370 4375 4380

Asp Gly Asp Val Phe Ala Glu Val Ala Leu Pro Glu Asp Leu Arg Lys
4385 4390 4395 4400

Asp Ala Gly Arg Phe Gly Val His Pro Ala Leu Leu Asp Ala Ala Leu
4405 4410 4415

Gln Ala Ala Thr Ala Val Gly Gly Asp Glu Pro Gly Gln Pro Val Leu
4420 4425 4430

Ala Phe Ala Trp Asn Gly Leu Val Leu His Ala Ala Gly Ala Ser Ala
4435 4440 4445

Leu Arg Val Arg Leu Ala Pro Ser Gly Pro Asp Thr Leu Ser Val Ala
4450 4455 4460

Ala Ala Asp Glu Thr Gly Gly Leu Val Leu Thr Met Glu Ser Leu Val
4465 4470 4475 4480

Ser Arg Pro Val Ser Ala Glu Gln Leu Gly Ala Ala Ala Asp Ala Gly
4485 4490 4495

20250103 15:53:46

His Asp Ala Met Phe Arg Val Asp Trp Thr Glu Leu Pro Ala Val Pro
4500 4505 4510

Arg Ala Glu Leu Pro Pro Trp Val Arg Ile Asp Thr Ala Asp Asp Val
4515 4520 4525

Ala Ala Leu Ala Glu Lys Ala Asp Ala Pro Pro Val Val Val Trp Glu
4530 4535 4540

Ala Ala Gly Gly Asp Pro Ala Leu Ala Val Ser Ser Arg Val Leu Glu
4545 4550 4555 4560

Ile Met Gln Ala Trp Leu Ala Ala Pro Ala Phe Glu Glu Ala Arg Leu
4565 4570 4575

Val Val Thr Thr Arg Gly Ala Val Pro Ala Gly Gly Asp His Thr Leu
4580 4585 4590

Thr Asp Pro Ala Ala Ala Ala Val Trp Gly Leu Val Arg Ser Ala Gln
4595 4600 4605

Ala Glu His Pro Asp Arg Val Val Leu Leu Asp Thr Asp Gly Glu Val
4610 4615 4620

Pro Leu Gly Ala Val Leu Ala Ser Gly Glu Pro Gln Leu Ala Val Arg
4625 4630 4635 4640

Gly Thr Thr Phe Phe Val Pro Arg Leu Ala Arg Ala Thr Arg Leu Ser
4645 4650 4655

Asp Ala Pro Pro Ala Phe Asp Pro Asp Gly Thr Val Leu Val Ser Gly
4660 4665 4670

Ala Gly Ser Leu Gly Thr Leu Val Ala Arg His Leu Val Thr Arg His
4675 4680 4685

Gly Val Arg Arg Val Val Leu Ala Ser Arg Gln Gly Arg Asp Ala Glu

4690	4695	4700
Gly Ala Gln Asp Leu Ile Thr Glu Leu Thr Gly Glu Gly Ala Asp Val		
4705	4710	4715 4720
Ser Phe Val Ala Cys Asp Val Ser Asp Arg Asp Gln Val Ala Ala Leu		
	4725	4730 4735
Leu Ala Gly Leu Pro Asp Leu Thr Gly Val Val His Thr Ala Gly Val		
	4740	4745 4750
Phe Glu Asp Gly Val Ile Glu Ala Leu Thr Pro Asp Gln Leu Ala Asn		
	4755	4760 4765
Val Tyr Ala Ala Lys Val Thr Ala Ala Met His Leu Asp Glu Leu Thr		
	4770	4775 4780
Arg Asp Arg Asp Leu Gly Ala Phe Val Val Phe Ser Ser Val Ala Gly		
4785	4790	4795 4800
Val Met Gly Gly Gly Gly Gln Gly Pro Tyr Ala Ala Ala Asn Ala Phe		
	4805	4810 4815
Leu Asp Ala Ala Met Ala Ser Arg Gln Ala Ala Gly Leu Pro Gly Leu		
	4820	4825 4830
Ser Leu Ala Trp Gly Leu Trp Glu Arg Ser Ser Gly Met Ala Ala His		
	4835	4840 4845
Leu Ser Glu Val Asp His Ala Arg Ala Ser Arg Asn Gly Val Leu Glu		
	4850	4855 4860
Leu Thr Arg Ala Glu Gly Leu Ala Leu Phe Asp Leu Gly Leu Arg Met		
4865	4870	4875 4880
Ala Glu Ser Leu Leu Val Pro Ile Lys Leu Asp Leu Ala Ala Met Arg		
	4885	4890 4895

Ala Ser Thr Val Pro Val Leu Phe Arg Gly Leu Val Arg Pro Ser Arg
4900 4905 4910

Thr Gln Ala Arg Thr Ala Ser Thr Val Asp Arg Gly Leu Ala Gly Arg
4915 4920 4925

Leu Ala Gly Leu Pro Val Ala Glu Arg Ala Ala Val Leu Val Asp Leu
4930 4935 4940

Val Arg Gly Gln Val Ala Val Val Leu Gly Tyr Asp Gly Pro Glu Ala
4945 4950 4955 4960

Val Arg Pro Asp Thr Ala Phe Lys Asp Thr Gly Phe Asp Ser Leu Thr
4965 4970 4975

Ser Val Glu Leu Arg Asn Arg Leu Arg Glu Ala Thr Gly Leu Lys Leu
4980 4985 4990

Pro Ala Thr Leu Val Phe Asp Tyr Pro Asn Pro Leu Ala Val Ala Arg
4995 5000 5005

Tyr Leu Gly Ala Arg Leu Val Pro Asp Gly Thr Ala Asn Gly Asn Gly
5010 5015 5020

Asn Gly Asn Gly His Ser Glu Asp Asp Arg Leu Arg His Ala Leu Ala
5025 5030 5035 5040

Ala Ile Ala Ala Glu Asp Ala Gly Glu Glu Arg Ser Ile Ala Asp Leu
5045 5050 5055

Gly Val Asp Asp Leu Val Gln Leu Ala Phe Gly Asp Glu
5060 5065

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1721 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Ala Cys Arg Leu Pro Gly Gly Val Thr Gly Pro Gly Asp Leu Trp
1 5 10 15

Arg Leu Val Ala Glu Gly Gly Asp Ala Val Ser Gly Phe Pro Thr Asp
 20 25 30

Arg Cys Trp Asp Leu Asp Thr Leu Phe Asp Pro Asp Pro Asp His Ala
 35 40 45

Gly Thr Ser Tyr Thr Asp Gln Gly Gly Phe Leu His Asp Ala Ala Leu
50 55 60

Phe Asp Pro Gly Phe Phe Gly Ile Ser Pro Arg Glu Ala Leu Ala Met
65 70 75 80

Asp Pro Gln Gln Arg Leu Leu Leu Glu Ala Ser Trp Glu Ala Leu Glu
 85 90 95

Gly Val Gly Leu Asp Pro Ala Ser Leu Gln Gly Thr Asp Val Gly Val
 100 105 110

Phe Thr Gly Ala Gly Gly Ser Gly Tyr Gly Gly Gly Leu Thr Gly Pro
 115 120 125

Glu Met Gln Ser Phe Ala Gly Thr Gly Leu Ala Ser Ser Val Ala Ser

130	135	140	
Gly Arg Val Ser Tyr Val Phe Gly Phe Glu Gly Pro Ala Val Thr Ile			
145	150	155	160
Asp Thr Ala Cys Ser Ser Ser Leu Val Ala Met His Leu Ala Ala Gln			
165	170	175	
Ala Leu Arg Gln Gly Asp Cys Ser Met Ala Leu Ala Gly Gly Ala Met			
180	185	190	
Val Met Ser Gly Pro Asp Ser Phe Val Val Phe Ser Arg Gln Arg Gly			
195	200	205	
Leu Ala Thr Asp Gly Arg Cys Lys Ala Phe Ala Ser Gly Ala Asp Gly			
210	215	220	
Met Val Leu Ala Glu Gly Ile Ser Val Val Val Leu Glu Arg Leu Ser			
225	230	235	240
Val Ala Arg Glu Arg Gly His Arg Val Leu Ala Val Leu Arg Gly Ser			
245	250	255	
Ala Val Asn Gln Asp Gly Ala Ser Asn Gly Leu Thr Ala Pro Asn Gly			
260	265	270	
Pro Ser Gln Gln Arg Val Ile Arg Ala Ala Leu Ala Asn Ala Gly Ile			
275	280	285	
Gly Pro Ser Asp Val Asp Leu Val Glu Ala His Gly Thr Gly Thr Ser			
290	295	300	
Leu Gly Asp Pro Ile Glu Ala Gln Ala Leu Leu Ala Thr Tyr Gly Gln			
305	310	315	320
Asp Arg Glu Thr Pro Leu Trp Leu Gly Ser Leu Lys Ser Asn Ile Gly			
325	330	335	

His Thr Gln Ala Ala Ala Gly Val Ala Ser Val Ile Lys Val Val Gln
340 345 350

Ala Leu Arg His Gly Val Met Pro Pro Thr Leu His Val Asp Glu Pro
355 360 365

Ser Ser Gln Val Asp Trp Ser Glu Gly Ala Val Glu Leu Leu Thr Gly
370 375 380

Ser Arg Asp Trp Pro Arg Gly Asp Arg Pro Arg Arg Ala Gly Val Ser
385 390 395 400

Ser Phe Gly Val Ser Gly Thr Asn Val His Leu Ile Ile Glu Glu Ala
405 410 415

Pro Glu Glu Pro Ala Ala Ala Val Pro Thr Ser Ala Asp Val Val Pro
420 425 430

Leu Val Val Ser Ala Arg Ser Thr Gly Ser Leu Ala Gly Gln Ala Asp
435 440 445

Arg Leu Thr Glu Val Asp Val Pro Leu Gly His Leu Ala Gly Ala Leu
450 455 460

Val Ala Gly Arg Ala Val Leu Glu Glu Arg Ala Val Val Val Ala Gly
465 470 475 480

Ser Ala Glu Glu Ala Arg Ala Gly Leu Gly Ala Leu Ala Arg Gly Glu
485 490 495

Ala Ala Pro Gly Val Val Thr Gly Thr Ala Gly Lys Pro Gly Lys Val
500 505 510

Val Trp Val Phe Pro Gly Gln Gly Thr Gln Trp Val Gly Met Gly Arg
515 520 525

Glu Leu Leu Asp Ala Ser Pro Val Phe Ala Glu Arg Ile Lys Glu Cys
530 535 540

Ala Ala Ala Leu Asp Gln Trp Thr Asp Trp Ser Leu Leu Asp Val Leu
545 550 555 560

Arg Gly Asp Gly Asp Leu Asp Ser Val Glu Val Leu Gln Pro Ala Cys
565 570 575

Phe Ala Val Met Val Gly Leu Ala Ala Val Trp Glu Ser Ala Gly Val
580 585 590

Arg Pro Asp Ala Val Val Gly His Ser Gln Gly Glu Ile Ala Ala Ala
595 600 605

Cys Val Ser Gly Ala Leu Thr Leu Asp Asp Ala Ala Lys Val Val Ala
610 615 620

Leu Arg Ser Gln Ala Ile Ala Ala Arg Leu Ser Gly Arg Gly Gly Met
625 630 635 640

Ala Ser Val Ala Leu Ser Glu Asp Glu Ala Asn Ala Arg Leu Gly Leu
645 650 655

Trp Asp Gly Arg Ile Glu Val Ala Ala Val Asn Gly Pro Ala Ser Val
660 665 670

Val Ile Ala Gly Asp Ala Gln Ala Leu Asp Glu Ala Leu Glu Val Leu
675 680 685

Ala Gly Asp Gly Val Arg Val Arg Gln Val Ala Val Asp Tyr Ala Ser
690 695 700

His Thr Arg His Val Glu Asp Ile Arg Asp Thr Leu Ala Glu Thr Leu
705 710 715 720

Ala Gly Ile Thr Ala Gln Ala Pro Asp Val Pro Phe Arg Ser Thr Val

725	730	735
Thr Gly Gly Trp Val Arg Asp Ala Asp Val Leu Asp Gly Gly Tyr Trp		
740	745	750
Tyr Arg Asn Leu Arg Asn Gln Val Arg Phe Gly Pro Ala Val Ala Glu		
755	760	765
Leu Leu Glu Gln Gly His Gly Val Phe Val Glu Val Ser Ala His Pro		
770	775	780
Val Leu Val Gln Pro Ile Ser Glu Leu Thr Asp Ala Val Val Thr Gly		
785	790	795 800
Thr Leu Arg Arg Asp Asp Gly Gly Leu Arg Arg Leu Leu Thr Ser Met		
805	810	815
Ala Glu Leu Phe Val Arg Gly Val Arg Val Asp Trp Ala Thr Leu Val		
820	825	830
Pro Pro Ala Arg Val Asp Leu Pro Thr Tyr Ala Phe Asp His Gln His		
835	840	845
Phe Trp Leu Arg Pro Ala Ala Gln Ala Asp Ala Val Ser Leu Gly Gln		
850	855	860
Ala Ala Ala Glu His Pro Leu Leu Gly Ala Val Val Arg Leu Pro Gln		
865	870	875 880
Ser Asp Gly Leu Val Phe Thr Ser Arg Leu Ser Leu Arg Thr His Pro		
885	890	895
Trp Leu Ala Asp His Thr Ile Gly Gly Val Val Leu Phe Pro Gly Thr		
900	905	910
Gly Leu Val Glu Leu Ala Val Arg Ala Gly Asp Glu Ala Gly Cys Pro		
915	920	925

Val Leu Asp Glu Leu Val Thr Glu Ala Pro Leu Val Val Pro Gly Gln
930 935 940

Gly Gly Val Asn Val Gln Val Thr Val Ser Gly Pro Asp Gln Asn Gly
945 950 955 960

Leu Arg Thr Val Asp Ile His Ser Gln Arg Asp Asp Val Trp Thr Arg
965 970 975

His Ala Thr Gly Thr Val Ser Ala Thr Pro Ala Ser Ser Pro Gly Phe
980 985 990

Asp Phe Thr Ala Trp Pro Pro Pro Asp Gly Gln Arg Val Glu Ile Gly
995 1000 1005

Asp Phe Tyr Ala Asp Leu Ala Glu Arg Gly Tyr Ala Tyr Gly Pro Leu
1010 1015 1020

Phe Gln Gly Val Arg Ala Val Trp Gln Arg Gly Glu Asp Val Phe Ala
1025 1030 1035 1040

Glu Val Ala Leu Pro Glu Asp Arg Arg Glu Asp Ala Ala Arg Phe Gly
1045 1050 1055

Leu His Pro Ala Leu Leu Asp Ala Ala Leu Gln Thr Gly Thr Ile Ala
1060 1065 1070

Ala Ala Ala Ser Gly Gln Pro Gly Lys Ser Val Met Pro Phe Ser Trp
1075 1080 1085

Asn Arg Leu Ala Leu His Ala Val Gly Ala Ala Gly Leu Arg Val Arg
1090 1095 1100

Val Ala Pro Gly Gly Pro Asp Ala Leu Thr Val Glu Ala Ala Asp Glu
1105 1110 1115 1120

Thr Gly Ala Pro Val Leu Thr Met Asp Ser Leu Ile Leu Arg Glu Val
1125 1130 1135

Ala Leu Asp Gln Leu Asp Thr Ala Arg Ala Gly Ser Leu Tyr Arg Val
1140 1145 1150

Asp Trp Thr Pro Leu Pro Thr Val Asp Ser Ala Val Pro Ala Gly Arg
1155 1160 1165

Ala Glu Val Leu Glu Ala Phe Gly Glu Glu Pro Leu Asp Leu Thr Gly
1170 1175 1180

Arg Val Leu Ala Ala Leu Gln Ala Trp Leu Ser Asp Ala Ala Glu Glu
1185 1190 1195 1200

Ala Arg Leu Val Val Val Thr Arg Gly Ala Val Pro Ala Gly Asp Gly
1205 1210 1215

Val Val Ser Asp Pro Ala Gly Ala Ala Val Trp Gly Leu Val Arg Ala
1220 1225 1230

Ala Gln Ala Glu Asn Pro Asp Arg Phe Val Leu Leu Asp Thr Asp Gly
1235 1240 1245

Glu Val Pro Leu Glu Ala Val Leu Ala Thr Gly Glu Pro Gln Leu Ala
1250 1255 1260

Leu Arg Gly Thr Thr Phe Ser Val Pro Arg Leu Ala Arg Val Thr Glu
1265 1270 1275 1280

Pro Ala Glu Ala Pro Leu Thr Phe Arg Pro Asp Gly Thr Val Leu Val
1285 1290 1295

Ser Gly Ala Gly Thr Leu Gly Ala Leu Ala Ala Arg Asp Leu Val Thr
1300 1305 1310

Arg His Gly Val Arg Arg Leu Val Leu Ala Ser Arg Arg Gly Arg Ala

1315	1320	1325
Ala Glu Gly Ile Asp Asp Leu Val Ala Glu Leu Thr Gly His Gly Ala		
1330	1335	1340
Glu Val Thr Val Ala Ala Cys Asp Val Ser Asp Arg Asp Gln Val Ala		
1345	1350	1355 1360
Ala Leu Leu Lys Glu His Ala Leu Thr Ala Val Val His Thr Ala Gly		
1365	1370	1375
Val Phe Asp Ala Gly Val Thr Gly Ala Leu Thr Arg Glu Arg Leu Ala		
1380	1385	1390
Lys Val Phe Ala Pro Lys Val Asp Ala Ala Asn His Leu Asp Glu Leu		
1395	1400	1405
Thr Arg Asp Leu Asp Leu Asp Ala Phe Ile Val Tyr Ser Ser Ala Ser		
1410	1415	1420
Ser Ile Phe Met Gly Ala Gly Ser Gly Gly Tyr Ala Ala Ala Asn Ala		
1425	1430	1435 1440
Tyr Leu Asp Gly Leu Met Ala Ala Arg Arg Ala Ala Gly Leu Pro Gly		
1445	1450	1455
Leu Ser Leu Ala Trp Gly Pro Trp Glu Gln Leu Thr Gly Met Ala Asp		
1460	1465	1470
Thr Ile Asp Asp Leu Thr Leu Ala Arg Met Ser Arg Arg Glu Gly Arg		
1475	1480	1485
Gly Gly Val Arg Ala Leu Gly Ser Ala Asp Gly Met Glu Leu Phe Asp		
1490	1495	1500
Ala Ala Leu Ala Ala Gly Gln Ala Leu Leu Val Pro Ile Glu Leu Asp		
1505	1510	1515 1520

Leu Arg Glu Val Arg Ala Asp Ala Ala Gly Gly Gly Thr Val Pro His
1525 1530 1535

Leu Leu Arg Gly Leu Val Arg Ala Gly Arg Gln Ala Ala Arg Thr Ala
1540 1545 1550

Ala Thr Glu Asp Gly Gly Leu Glu Arg Arg Leu Ala Gly Leu Thr Val
1555 1560 1565

Ala Glu Gln Glu Ala Leu Leu Leu Asp Leu Val Arg Gly Gln Val Ala
1570 1575 1580

Val Val Leu Gly His Ala Asp Ser Ser Gly Val Arg Ala Asp Ala Ala
1585 1590 1595 1600

Phe Lys Asp Ala Gly Phe Asp Ser Leu Thr Ser Val Glu Leu Arg Asn
1605 1610 1615

Arg Leu Arg Glu Thr Thr Gly Leu Lys Leu Pro Ala Thr Leu Val Phe
1620 1625 1630

Asp His Pro Asn Pro Leu Ala Leu Ala Arg His Leu Arg Ala Glu Leu
1635 1640 1645

Ala Val Asp Glu Ala Ser Pro Ala Asp Ala Val Leu Ala Gly Leu Ala
1650 1655 1660

Gly Leu Glu Ala Ala Ile Ala Ala Ala Gly Ala Pro Asp Gly Asp Arg
1665 1670 1675 1680

Ile Thr Ala Arg Leu Arg Glu Leu Leu Lys Ala Ala Glu Ala Ala Glu
1685 1690 1695

Ala Arg Pro Gly Thr Ser Gly Asp Leu Asp Thr Ala Ser Asp Glu Glu
1700 1705 1710

Leu Phe Ala Leu Val Asp Gly Leu Asp
1715 1720

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1688 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Met Ala Cys Arg Tyr Pro Gly Gly Val Ser Ser Pro Glu Asp Leu Trp
1 5 10 15

Arg Leu Val Ala Glu Gly Thr Asp Ala Val Ser Ala Phe Pro Gly Asp
20 25 30

Arg Gly Trp Asp Val Asp Gly Leu Val Asp Pro Asp Pro Asp Arg Pro
35 40 45

Gly Thr Thr Tyr Thr Asp Gln Gly Gly Phe Leu His Glu Ala Gly Leu
50 55 60

Phe Asp Ala Gly Phe Phe Gly Ile Ser Pro Arg Glu Ala Val Ala Met
65 70 75 80

Asp Pro Gln Gln Arg Leu Leu Leu Glu Thr Ser Trp Glu Ala Ile Glu
85 90 95

Arg Thr Gly Thr Asp Pro Leu Ser Leu Lys Gly Ser Asp Ile Gly Val

$\frac{1}{\sqrt{\pi}} \int_{-\infty}^{\infty} f(x) e^{-ixy} dx = g(y)$

Thr Thr Leu Gly Asp Pro Ile Glu Ala Gln Ala Leu Leu Ala Thr Tyr
305 310 315 320

Gly Lys Gly Arg Asp Pro Glu Lys Pro Leu Trp Leu Gly Ser Val Lys
325 330 335

Ser Asn Leu Gly His Thr Gln Ala Ala Ala Gly Val Ala Ser Val Ile
340 345 350

Lys Met Val Gln Ala Leu Arg His Gly Val Leu Pro Pro Thr Leu His
355 360 365

Val Asp Arg Pro Ser Thr Glu Val Asp Trp Ser Ala Gly Ala Val Ser
370 375 380

Leu Leu Thr Glu Ala Arg Glu Trp Pro Arg Glu Gly Arg Pro Arg Arg
385 390 395 400

Ala Gly Val Ser Ser Phe Gly Ile Ser Gly Thr Asn Ala His Leu Ile
405 410 415

Leu Glu Glu Ala Pro Glu Glu Glu Pro Pro Val Ala Glu Ala Pro Ser
420 425 430

Ala Gly Val Val Pro Val Val Val Ser Ala Arg Gly Ala Leu Ala Gly
435 440 445

Gln Ala Gly Arg Leu Ala Ala Phe Leu Glu Ala Ser Asp Glu Pro Leu
450 455 460

Val Thr Val Ala Gly Ala Leu Ile Cys Gly Arg Ser Arg Phe Gly Asp
465 470 475 480

Arg Ala Val Val Val Ala Gly Thr Arg Ala Glu Ala Thr Ala Gly Leu
485 490 495

2060534004

Ala Ala Leu Ala Arg Gly Glu Ser Ala Ala Asp Val Val Thr Gly Thr
500 505 510

Val Ala Ala Ser Gly Val Pro Gly Lys Leu Val Trp Val Phe Pro Gly
515 520 525

Gln Gly Ser Gln Trp Val Gly Met Gly Arg Glu Leu Leu Glu Ala Ser
530 535 540

Pro Val Phe Ala Ala Arg Ile Ala Glu Cys Ala Ala Ala Leu Glu Pro
545 550 555 560

Trp Ile Asp Trp Ser Leu Leu Asp Val Leu Arg Gly Glu Gly Asp Leu
565 570 575

Asp Arg Val Asp Val Val Gln Pro Ala Ser Phe Ala Val Met Val Gly
580 585 590

Leu Ala Ala Val Trp Ser Ser Val Gly Val Val Pro Asp Ala Val Leu
595 600 605

Gly His Ser Gln Gly Glu Ile Ala Ala Ala Cys Val Ser Gly Ala Leu
610 615 620

Ser Leu Gln Asp Ala Ala Lys Val Val Ala Leu Arg Ser Gln Ala Ile
625 630 635 640

Ala Ala Lys Leu Ala Gly Arg Gly Gly Met Ala Ser Val Ala Leu Ser
645 650 655

Glu Glu Asp Ala Val Ala Arg Leu Arg His Trp Ala Asp Arg Val Glu
660 665 670

Val Ala Ala Val Asn Ser Pro Ser Ser Val Val Ile Ala Gly Asp Ala
675 680 685

Glu Ala Leu Asp Gln Ala Leu Glu Ala Leu Thr Gly Gln Asp Ile Arg

690 695 700

Val Arg Arg Val Ala Val Asp Tyr Ala Ser His Thr Arg His Val Glu
705 710 715 720

Asp Ile Gln Glu Pro Leu Ala Glu Ala Leu Ala Gly Ile Glu Ala His
725 730 735

Ala Pro Thr Leu Pro Phe Phe Ser Thr Leu Thr Gly Asp Trp Ile Arg
740 745 750

Glu Ala Gly Val Val Asp Gly Gly Tyr Trp Tyr Arg Asn Leu Arg Asn
755 760 765

Gln Val Gly Phe Gly Pro Ala Val Ala Glu Leu Leu Gly Leu Gly His
770 775 780

Arg Val Phe Val Glu Val Ser Ala His Pro Val Leu Val Gln Ala Ile
785 790 795 800

Ser Ala Ile Ala Asp Asp Thr Asp Ala Val Val Thr Gly Ser Leu Arg
805 810 815

Arg Glu Glu Gly Gly Leu Arg Arg Leu Leu Thr Ser Met Ala Glu Leu
820 825 830

Phe Val Arg Gly Val Asp Val Asp Trp Ala Thr Met Val Pro Pro Ala
835 840 845

Arg Val Asp Leu Pro Thr Tyr Ala Phe Asp His Gln His Tyr Trp Leu
850 855 860

Arg Tyr Val Glu Thr Ala Thr Asp Ala Ala Gly Pro Val Val Arg Leu
865 870 875 880

Pro Gln Thr Gly Gly Leu Val Phe Thr Thr Glu Trp Ser Leu Lys Ser
885 890 895

206000593400

Gln Pro Trp Leu Ala Glu His Thr Leu Glu Asp Leu Val Val Val Pro
900 905 910

Gly Ala Ala Leu Val Glu Leu Ala Val Arg Ala Gly Asp Glu Ala Gly
915 920 925

Thr Pro Val Leu Asp Glu Leu Val Ile Glu Thr Pro Leu Val Val Pro
930 935 940

Glu Arg Gly Ala Ile Arg Val Gln Val Thr Val Ser Gly Pro Asp Asp
945 950 955 960

Gly Thr Arg Thr Leu Glu Val His Ser Gln Pro Glu Asp Ala Thr Asp
965 970 975

Glu Trp Thr Arg His Ala Thr Gly Thr Leu Ser Ala Thr Pro Asp Glu
980 985 990

Ser Ser Gly Phe Asp Phe Thr Ala Trp Pro Pro Pro Gly Ala Arg Gln
995 1000 1005

Leu Asp Gly Val Pro Ala Ile Trp Arg Ala Gly Asp Glu Ile Phe Ala
1010 1015 1020

Glu Val Ser Leu Pro Asp Asp Ala Asp Ala Glu Ala Phe Gly Ile His
1025 1030 1035 1040

Pro Ala Leu Leu Asp Ala Ala Leu His Pro Ala Leu Pro Gly Asp Asp
1045 1050 1055

Gly Leu Thr Gln Pro Met Glu Trp Arg Gly Leu Thr Leu His Ala Ala
1060 1065 1070

Gly Ala Ser Thr Leu Arg Val Arg Leu Val Pro Gly Gly Phe Leu Glu
1075 1080 1085

20250329 15:04:00

Ala Ala Asp Gly Ala Gly Ser Leu Val Val Thr Ala Lys Glu Val Ala
1090 1095 1100

Leu Arg Pro Val Thr Ile Ala Arg Ser Arg Thr Thr Thr Arg Asp Ser
1105 1110 1115 1120

Leu Phe Gln Leu Asn Trp Ile Glu Leu Pro Glu Ser Gly Val Val Ala
1125 1130 1135

Ala Ala Asp Asp Thr Glu Val Leu Glu Val Pro Ala Gly Asp Ser Pro
1140 1145 1150

Leu Ala Ala Thr Ser Arg Val Leu Glu Arg Leu Gln Thr Trp Leu Thr
1155 1160 1165

Glu Pro Glu Ala Glu Gln Leu Val Val Val Thr Arg Gly Ala Val Pro
1170 1175 1180

Ala Gly Asp Thr Pro Val Thr Asp Pro Ala Ala Ala Val Trp Gly
1185 1190 1195 1200

Leu Val Arg Ser Ala Gln Ala Glu Asn Pro Asp Arg Ile Val Leu Leu
1205 1210 1215

Asp Thr Asp Gly Glu Val Pro Leu Gly Ala Val Leu Ala Gly Gly Glu
1220 1225 1230

Pro Gln Val Ala Val Arg Gly Thr Ala Leu Tyr Val Pro Arg Leu Ala
1235 1240 1245

Arg Ala Asp Ala Ala Pro Val Ser Gly Leu His Gly Thr Val Leu Val
1250 1255 1260

Ser Gly Ala Gly Val Leu Gly Glu Ile Val Ala Arg His Leu Val Thr
1265 1270 1275 1280

Arg His Gly Val Arg Lys Leu Val Leu Ala Ser Arg Arg Gly Leu Asp

1280 1285 1290 1295 1300 1305 1310 1315 1320 1325 1330 1335 1340 1345 1350 1355 1360 1365 1370 1375 1380 1385 1390 1395 1400 1405 1410 1415 1420 1425 1430 1435 1440 1445 1450 1455 1460 1465 1470 1475 1480 1485 1490 1495 1500 1505 1510 1515 1520 1525 1530 1535 1540 1545 1550 1555 1560 1565 1570 1575 1580 1585 1590 1595 1600 1605 1610 1615 1620 1625 1630 1635 1640 1645 1650 1655 1660 1665 1670 1675 1680 1685 1690 1695 1700 1705 1710 1715 1720 1725 1730 1735 1740 1745 1750 1755 1760 1765 1770 1775 1780 1785 1790 1795 1800 1805 1810 1815 1820 1825 1830 1835 1840 1845 1850 1855 1860 1865 1870 1875 1880 1885 1890 1895 1900 1905 1910 1915 1920 1925 1930 1935 1940 1945 1950 1955 1960 1965 1970 1975 1980 1985 1990 1995 2000

1285	1290	1295
Ala Asp Gly Ala Lys Asp Leu Val Thr Asp Leu Thr Gly Glu Gly Ala		
1300	1305	1310
Asp Val Ser Val Val Ala Cys Asp Leu Ala Asp Arg Asn Gln Val Ala		
1315	1320	1325
Ala Leu Leu Ala Asp His Arg Pro Ala Ser Val Ile His Thr Ala Gly		
1330	1335	1340
Val Leu Asp Asp Gly Val Ile Gly Thr Leu Thr Pro Glu Arg Leu Ala		
1345	1350	1355 1360
Lys Val Phe Ala Pro Lys Val Asp Ala Val Arg His Leu Asp Glu Leu		
1365	1370	1375
Thr Arg Asp Leu Asp Leu Asp Ala Phe Val Val Phe Ser Ser Gly Ser		
1380	1385	1390
Gly Val Phe Gly Ser Pro Gly Gln Gly Asn Tyr Ala Ala Ala Asn Ala		
1395	1400	1405
Phe Leu Asp Ala Ala Met Ala Ser Arg Arg Ala Ala Gly Leu Pro Gly		
1410	1415	1420
Leu Ser Leu Ala Trp Gly Leu Trp Glu Gln Ala Thr Gly Met Thr Ala		
1425	1430	1435 1440
His Leu Gly Gly Thr Asp Gln Ala Arg Met Ser Arg Gly Gly Val Arg		
1445	1450	1455
Pro Ile Thr Ala Glu Glu Gly Met Ala Leu Phe Asp Thr Ala Leu Gly		
1460	1465	1470
Ala Gln Pro Ala Leu Leu Val Pro Val Lys Leu Asp Leu Arg Glu Val		
1475	1480	1485

20250405 15:00:00

Arg Ala Gly Gly Ala Val Pro His Leu Leu Arg Gly Leu Val Arg Ala
1490 1495 1500

Gly Arg Arg Gln Ala Gln Ala Ala Ser Thr Val Asp Asn Gln Leu Leu
1505 1510 1515 1520

Gly Arg Leu Ala Gly Leu Gly Ala Pro Glu Gln Glu Ala Leu Leu Val
1525 1530 1535

Asp Leu Val Arg Gly Gln Val Ala Ala Val Leu Gly His Ala Gly Pro
1540 1545 1550

Asp Ala Val Arg Ala Asp Thr Ala Phe Lys Asp Ala Gly Phe Asp Ser
1555 1560 1565

Leu Thr Ser Val Asp Leu Arg Asn Arg Leu Arg Glu Ser Thr Gly Leu
1570 1575 1580

Lys Leu Pro Ala Thr Leu Ala Phe Asp Tyr Pro Thr Pro Leu Val Leu
1585 1590 1595 1600

Ala Arg His Leu Arg Asp Glu Leu Gly Ala Gly Asp Asp Ala Leu Ser
1605 1610 1615

Val Val His Ala Arg Leu Glu Asp Val Glu Ala Leu Leu Gly Gly Leu
1620 1625 1630

Arg Leu Asp Glu Ser Thr Lys Thr Gly Leu Thr Leu Arg Leu Gln Gly
1635 1640 1645

Leu Val Ala Arg Cys Asn Gly Val Asn Asp Gln Thr Gly Gly Glu Thr
1650 1655 1660

Leu Ala Asp Arg Leu Glu Ala Ala Ser Ala Asp Glu Val Leu Asp Phe
1665 1670 1675 1680

2060F "52340F

Ile Asp Glu Glu Leu Gly Leu Thr

1685

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3413 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Ala Thr Asp Glu Lys Leu Leu Lys Tyr Leu Lys Arg Val Thr Ala
1 5 10 15

Glu Leu His Ser Leu Arg Lys Gln Gly Ala Arg His Ala Asp Glu Pro
20 25 30

Leu Ala Val Val Gly Met Ala Cys Arg Phe Pro Gly Gly Val Ser Ser
35 40 45

Pro Glu Asp Leu Trp Gln Leu Val Ala Gly Gly Val Asp Ala Leu Ser
50 55 60

Asp Phe Pro Asp Asp Arg Gly Trp Glu Leu Asp Gly Leu Phe Asp Pro
65 70 75 80

Asp Pro Asp His Pro Gly Thr Ser Tyr Thr Ser Gln Gly Gly Phe Leu
85 90 95

Arg Gly Ala Gly Leu Phe Asp Ala Gly Leu Phe Gly Ile Ser Pro Arg

100	105	110
Glu Ala Leu Val Met Asp Pro Gln Gln Arg Val Leu Leu Glu Thr Ser		
115	120	125
Trp Glu Ala Leu Glu Asp Ala Gly Val Asp Pro Leu Ser Leu Lys Gly		
130	135	140
Ser Asp Val Gly Val Phe Ser Gly Val Phe Thr Gln Gly Tyr Gly Ala		
145	150	155 160
Gly Ala Ile Thr Pro Asp Leu Glu Ala Phe Ala Gly Ile Gly Ala Ala		
165	170	175
Ser Ser Val Ala Ser Gly Arg Val Ser Tyr Val Phe Gly Leu Glu Gly		
180	185	190
Pro Ala Val Thr Ile Asp Thr Ala Cys Ser Ser Ser Leu Val Ala Ile		
195	200	205
His Leu Ala Ala Gln Ala Leu Arg Ala Gly Glu Cys Ser Met Ala Leu		
210	215	220
Ala Gly Gly Ala Thr Val Met Pro Thr Pro Gly Thr Phe Val Ala Phe		
225	230	235 240
Ser Arg Gln Arg Val Leu Ala Ala Asp Gly Arg Ser Lys Ala Phe Ser		
245	250	255
Ser Thr Ala Asp Gly Thr Gly Trp Ala Glu Gly Ala Gly Val Leu Val		
260	265	270
Leu Glu Arg Leu Ser Val Ala Gln Glu Arg Gly His Arg Ile Leu Ala		
275	280	285
Val Leu Arg Gly Ser Ala Val Asn Gln Asp Gly Ala Ser Asn Gly Leu		
290	295	300

20609 " 33400"

Thr Ala Pro Asn Gly Pro Ser Gln Gln Arg Val Ile Arg Lys Ala Leu
305 310 315 320

Ala Gly Ala Gly Leu Val Ala Ser Asp Val Asp Val Val Glu Ala His
325 330 335

Gly Thr Gly Thr Ala Leu Gly Asp Pro Ile Glu Ala Gln Ala Leu Leu
340 345 350

Ala Thr Tyr Gly Gln Gly Arg Glu Arg Pro Leu Trp Leu Gly Ser Val
355 360 365

Lys Ser Asn Phe Gly His Thr Gln Ala Ala Ala Gly Val Ala Gly Val
370 375 380

Ile Lys Met Val Gln Ala Leu Arg His Gly Ala Met Pro Pro Thr Leu
385 390 395 400

His Val Ala Glu Pro Thr Pro Glu Val Asp Trp Ser Ala Gly Ala Val
405 410 415

Glu Leu Leu Thr Glu Pro Arg Glu Trp Pro Ala Gly Asp Arg Pro Arg
420 425 430

Arg Ala Gly Val Ser Ala Phe Gly Ile Ser Gly Thr Asn Ala His Leu
435 440 445

Ile Leu Glu Glu Ala Pro Pro Ala Asp Ala Val Ala Glu Glu Pro Glu
450 455 460

Phe Lys Gly Pro Val Pro Leu Val Val Ser Ala Gly Ser Pro Thr Ser
465 470 475 480

Leu Ala Ala Gln Ala Gly Arg Leu Ala Glu Val Leu Ala Ser Gly Gly
485 490 495

20607033400F

Met Val Ala Val Ala Ala Ser Glu Ala Glu Val Ala Glu Leu Leu Gly

690	695	700
Asp Gly Val Glu Leu Ala Ala Val Asn Gly Pro Ser Ala Val Val Leu		
705	710	715 720
Ser Gly Asp Ala Asp Ala Val Val Ala Ala Ala Ala Arg Met Arg Glu		
725	730	735
Arg Gly His Lys Thr Lys Gln Leu Lys Val Ser His Ala Phe His Ser		
740	745	750
Ala Arg Met Ala Pro Met Leu Ala Glu Phe Ala Ala Glu Leu Ala Gly		
755	760	765
Val Thr Trp Arg Glu Pro Glu Ile Pro Val Val Ser Asn Val Thr Gly		
770	775	780
Arg Phe Ala Glu Pro Gly Glu Leu Thr Glu Pro Gly Tyr Trp Ala Glu		
785	790	795 800
His Val Arg Arg Pro Val Arg Phe Ala Glu Gly Val Ala Ala Ala Thr		
805	810	815
Glu Ser Gly Gly Ser Leu Phe Val Glu Leu Gly Pro Gly Ala Ala Leu		
820	825	830
Thr Ala Leu Val Glu Glu Thr Ala Glu Val Thr Cys Val Ala Ala Leu		
835	840	845
Arg Asp Asp Arg Pro Glu Val Thr Ala Leu Ile Thr Ala Val Ala Glu		
850	855	860
Leu Phe Val Arg Gly Val Ala Val Asp Trp Pro Ala Leu Leu Pro Pro		
865	870	875 880
Val Thr Gly Phe Val Asp Leu Pro Lys Tyr Ala Phe Asp Gln Gln His		
885	890	895

Ala Tyr Gly Pro Ser Phe Arg Gly Leu Arg Ala Val Trp Arg Arg Gly
1075 1080 1085

Asp Glu Val Phe Ala Glu Val Ala Leu Ala Glu Asp Asp Arg Ala Asp
1090 1095 1100

Ala Ala Arg Phe Gly Ile His Pro Gly Leu Leu Asp Ala Ala Leu His
1105 1110 1115 1120

Ala Gly Met Ala Gly Ala Thr Thr Thr Glu Glu Pro Gly Arg Pro Val
1125 1130 1135

Leu Pro Phe Ala Trp Asn Gly Leu Val Leu His Ala Ala Gly Ala Ser
1140 1145 1150

Ala Leu Arg Val Arg Leu Ala Pro Ser Gly Pro Asp Ala Leu Ser Val
1155 1160 1165

Glu Ala Ala Asp Glu Ala Gly Gly Leu Val Val Thr Ala Asp Ser Leu
1170 1175 1180

Val Ser Arg Pro Val Ser Ala Glu Gln Leu Gly Ala Ala Ala Asn His
1185 1190 1195 1200

Asp Ala Leu Phe Arg Val Glu Trp Thr Glu Ile Ser Ser Ala Gly Asp
1205 1210 1215

Val Pro Ala Asp His Val Glu Val Leu Glu Ala Val Gly Glu Asp Pro
1220 1225 1230

Leu Glu Leu Thr Gly Arg Val Leu Glu Ala Val Gln Thr Trp Leu Ala
1235 1240 1245

Asp Ala Ala Asp Asp Ala Arg Leu Val Val Val Thr Arg Gly Ala Val
1250 1255 1260

His Glu Val Thr Asp Pro Ala Gly Ala Ala Val Trp Gly Leu Ile Arg
1265 1270 1275 1280

Ala Ala Gln Ala Glu Asn Pro Asp Arg Ile Val Leu Leu Asp Thr Asp

1295

1300

1305

1310

1315

1320

1325

1330

1335

1340

1345

1350

1355

1360

1365

1370

1375

1380

1385

1390

1395

1400

1405

1410

1415

1420

1425

1430

1435

1440

1445

1450

1455

1460

1465

1470

1475

1480

1485

[illegible]

Asp Ala Val Val Ala Asn Arg Arg Ala Ala Gly Leu Pro Gly Thr Ser
1490 1495 1500

Leu Ala Trp Gly Leu Trp Glu Gln Thr Asp Gly Met Thr Ala His Leu
1505 1510 1515 1520

Gly Asp Ala Asp Gln Ala Arg Ala Ser Arg Gly Gly Val Leu Ala Ile
1525 1530 1535

Ser Pro Ala Glu Gly Met Glu Leu Phe Asp Ala Ala Pro Asp Gly Leu
1540 1545 1550

Val Val Pro Val Lys Leu Asp Leu Arg Lys Thr Arg Ala Gly Gly Thr
1555 1560 1565

Val Pro His Leu Leu Arg Gly Leu Val Arg Pro Gly Arg Gln Gln Ala
1570 1575 1580

Arg Pro Ala Ser Thr Val Asp Asn Gly Leu Ala Gly Arg Leu Ala Gly
1585 1590 1595 1600

Leu Ala Pro Ala Glu Gln Glu Ala Leu Leu Leu Asp Val Val Arg Thr
1605 1610 1615

Gln Val Ala Leu Val Leu Gly His Ala Gly Pro Glu Ala Val Arg Ala
1620 1625 1630

Asp Thr Ala Phe Lys Asp Thr Gly Phe Asp Ser Leu Thr Ser Val Glu
1635 1640 1645

Leu Arg Asn Arg Leu Arg Glu Ala Ser Gly Leu Lys Leu Pro Ala Thr
1650 1655 1660

Leu Val Phe Asp Tyr Pro Thr Pro Val Ala Leu Ala Arg Tyr Leu Arg
1665 1670 1675 1680

Asp Glu Leu Gly Asp Thr Val Ala Thr Thr Pro Val Ala Thr Ala Ala
1685 1690 1695

Ala Ala Asp Ala Gly Glu Pro Ile Ala Ile Val Gly Met Ala Cys Arg
1700 1705 1710

Leu Pro Gly Gly Val Thr Asp Pro Glu Gly Leu Trp Arg Leu Val Arg
1715 1720 1725

Asp Gly Leu Glu Gly Leu Ser Pro Phe Pro Glu Asp Arg Gly Trp Asp
1730 1735 1740

Leu Glu Asn Leu Phe Asp Asp Asp Pro Asp Arg Ser Gly Thr Thr Tyr
1745 1750 1755 1760

Thr Ser Arg Gly Gly Phe Leu Asp Gly Ala Gly Leu Phe Asp Ala Gly
1765 1770 1775

Phe Phe Gly Ile Ser Pro Arg Glu Ala Leu Ala Met Asp Pro Gln Gln
1780 1785 1790

Arg Leu Leu Leu Glu Ala Ala Trp Glu Ala Leu Glu Gly Thr Gly Val
1795 1800 1805

Asp Pro Gly Ser Leu Lys Gly Ala Asp Val Gly Val Phe Ala Gly Val
1810 1815 1820

Ser Asn Gln Gly Tyr Gly Met Gly Ala Asp Pro Ala Glu Leu Ala Gly
1825 1830 1835 1840

Tyr Ala Ser Thr Ala Gly Ala Ser Ser Val Val Ser Gly Arg Val Ser
1845 1850 1855

Tyr Val Phe Gly Phe Glu Gly Pro Ala Val Thr Ile Asp Thr Ala Cys
1860 1865 1870

Ser Ser Ser Leu Val Ala Met His Leu Ala Gly Gln Ala Leu Arg Gln

1875	1880	1885
Gly Glu Cys Ser Met Ala Leu Ala Gly Gly Val Thr Val Met Gly Thr		
1890	1895	1900
Pro Gly Thr Phe Val Glu Phe Ala Lys Gln Arg Gly Leu Ala Gly Asp		
1905	1910	1915 1920
Gly Arg Cys Lys Ala Tyr Ala Glu Gly Ala Asp Gly Thr Gly Trp Ala		
1925	1930	1935
Glu Gly Val Gly Val Val Val Leu Glu Arg Leu Ser Val Ala Arg Glu		
1940	1945	1950
Arg Gly His Arg Val Leu Ala Val Leu Arg Gly Ser Ala Val Asn Ser		
1955	1960	1965
Asp Gly Ala Ser Asn Gly Leu Thr Ala Pro Asn Gly Pro Ser Gln Gln		
1970	1975	1980
Arg Val Ile Arg Arg Ala Leu Ala Gly Ala Gly Leu Glu Pro Ser Asp		
1985	1990	1995 2000
Val Asp Ile Val Glu Gly His Gly Thr Gly Thr Ala Leu Gly Asp Pro		
2005	2010	2015
Ile Glu Ala Gln Ala Leu Leu Ala Thr Tyr Gly Lys Asp Arg Asp Pro		
2020	2025	2030
Glu Thr Pro Leu Trp Leu Gly Ser Val Lys Ser Asn Phe Gly His Thr		
2035	2040	2045
Gln Ser Ala Ala Gly Val Ala Gly Val Ile Lys Met Val Gln Ala Leu		
2050	2055	2060
Arg His Gly Val Met Pro Pro Thr Leu His Val Asp Arg Pro Thr Ser		
2065	2070	2075 2080

1004505040502000

Gln Val Asp Trp Ser Ala Gly Ala Val Glu Val Leu Thr Glu Ala Arg
2085 2090 2095

Glu Trp Pro Arg Asn Gly Arg Pro Arg Arg Ala Gly Val Ser Ser Phe
2100 2105 2110

Gly Ile Ser Gly Thr Asn Ala His Leu Ile Ile Glu Glu Ala Pro Ala
2115 2120 2125

Glu Pro Gln Leu Ala Gly Pro Pro Pro Asp Gly Gly Val Val Pro Leu
2130 2135 2140

Val Val Ser Ala Arg Ser Pro Gly Ala Leu Ala Gly Gln Ala Arg Arg
2145 2150 2155 2160

Leu Ala Thr Phe Leu Gly Asp Gly Pro Leu Ser Asp Val Ala Gly Ala
2165 2170 2175

Leu Thr Ser Arg Ala Leu Phe Gly Glu Arg Ala Val Val Val Ala Asp
2180 2185 2190

Ser Ala Glu Glu Ala Arg Ala Gly Leu Gly Ala Leu Ala Arg Gly Glu
2195 2200 2205

Asp Ala Pro Gly Leu Val Arg Gly Arg Val Pro Ala Ser Gly Leu Pro
2210 2215 2220

Gly Lys Leu Val Trp Val Phe Pro Gly Gln Gly Thr Gln Trp Val Gly
2225 2230 2235 2240

Met Gly Arg Glu Leu Leu Glu Glu Ser Pro Val Phe Ala Glu Arg Ile
2245 2250 2255

Ala Glu Cys Ala Ala Ala Leu Glu Pro Trp Ile Gly Trp Ser Leu Phe
2260 2265 2270

2085 2090 2095 2100 2105 2110 2115 2120 2125 2130 2135 2140 2145 2150 2155 2160 2165 2170 2175 2180 2185 2190 2195 2200 2205 2210 2215 2220 2225 2230 2235 2240 2245 2250 2255 2260 2265 2270

Asp Val Leu Arg Gly Asp Gly Asp Leu Asp Arg Val Asp Val Leu Gln
2275 2280 2285

Pro Ala Cys Phe Ala Val Met Val Gly Leu Ala Ala Val Trp Ser Ser
2290 2295 2300

Ala Gly Val Val Pro Asp Ala Val Leu Gly His Ser Gln Gly Glu Ile
2305 2310 2315 2320

Ala Ala Ala Cys Val Ser Gly Ala Leu Ser Leu Glu Asp Ala Ala Lys
2325 2330 2335

Val Val Ala Leu Arg Ser Gln Ala Ile Ala Ala Lys Leu Ser Gly Arg
2340 2345 2350

Gly Gly Met Ala Ser Val Ala Leu Gly Glu Ala Asp Val Val Ser Arg
2355 2360 2365

Leu Ala Asp Gly Val Glu Val Ala Ala Val Asn Gly Pro Ala Ser Val
2370 2375 2380

Val Ile Ala Gly Asp Ala Gln Ala Leu Asp Glu Thr Leu Glu Ala Leu
2385 2390 2395 2400

Ser Gly Ala Gly Ile Arg Ala Arg Arg Val Ala Val Asp Tyr Ala Ser
2405 2410 2415

His Thr Arg His Val Glu Asp Ile Glu Asp Thr Leu Ala Glu Ala Leu
2420 2425 2430

Ala Gly Ile Asp Ala Arg Ala Pro Leu Val Pro Phe Leu Ser Thr Leu
2435 2440 2445

Thr Gly Glu Trp Ile Arg Asp Glu Gly Val Val Asp Gly Gly Tyr Trp
2450 2455 2460

Tyr Arg Asn Leu Arg Gly Arg Val Arg Phe Gly Pro Ala Val Glu Ala

2465	2470	2475	2480
Leu Leu Ala Gln Gly His Gly Val Phe Val Glu Leu Ser Ala His Pro			
2485	2490	2495	
Val Leu Val Gln Pro Ile Thr Glu Leu Thr Asp Glu Thr Ala Ala Val			
2500	2505	2510	
Val Thr Gly Ser Leu Arg Arg Asp Asp Gly Gly Leu Arg Arg Leu Leu			
2515	2520	2525	
Thr Ser Met Ala Glu Leu Phe Val Arg Gly Val Glu Val Asp Trp Thr			
2530	2535	2540	
Ser Leu Val Pro Pro Ala Arg Ala Asp Leu Pro Thr Tyr Ala Phe Asp			
2545	2550	2555	2560
His Glu His Tyr Trp Leu Arg Ala Ala Asp Thr Ala Ser Asp Ala Val			
2565	2570	2575	
Ser Leu Gly Leu Ala Gly Ala Asp His Pro Leu Leu Gly Ala Val Val			
2580	2585	2590	
Gln Leu Pro Gln Ser Asp Gly Leu Val Phe Thr Ser Arg Leu Ser Leu			
2595	2600	2605	
Arg Ser His Pro Trp Leu Ala Asp His Ala Val Arg Asp Val Val Ile			
2610	2615	2620	
Val Pro Gly Thr Gly Leu Val Glu Leu Ala Val Arg Ala Gly Asp Glu			
2625	2630	2635	2640
Ala Gly Cys Pro Val Leu Asp Glu Leu Val Ile Glu Ala Pro Leu Val			
2645	2650	2655	
Val Pro Arg Arg Gly Gly Val Arg Val Gln Val Ala Leu Gly Gly Pro			
2660	2665	2670	

Gly Leu Val Val Thr Leu Asp Ser Leu Val Gly Arg Pro Val Ser Asn
2850 2855 2860

Asp Gln Leu Thr Thr Ala Ala Gly Pro Ala Gly Ala Gly Ser Leu Tyr
2865 2870 2875 2880

Arg Val Asp Trp Thr Pro Leu Ser Ser Val Asp Thr Ser Gly Arg Val
2885 2890 2895

Pro Ser Trp Leu Pro Val Ala Thr Ala Glu Glu Val Ala Thr Leu Ala
2900 2905 2910

Asp Asp Val Leu Thr Gly Ala Thr Glu Ala Pro Ala Val Ala Val Met
2915 2920 2925

Glu Ala Val Ala Asp Glu Gly Ser Val Leu Ala Leu Thr Val Arg Val
2930 2935 2940

Leu Asp Val Val Gln Cys Trp Leu Ala Gly Gly Gly Leu Glu Gly Thr
2945 2950 2955 2960

Lys Leu Ala Ile Val Thr Arg Gly Ala Val Pro Ala Gly Asp Gly Val
2965 2970 2975

Val His Asp Pro Ala Ala Ala Ala Val Trp Gly Leu Val Arg Ala Ala
2980 2985 2990

Gln Ala Glu Asn Pro Asp Arg Ile Val Leu Leu Asp Val Glu Pro Glu
2995 3000 3005

Ala Asp Val Pro Pro Leu Leu Gly Ser Val Leu Ala Asp Gly Glu Pro
3010 3015 3020

Gln Val Ala Val Arg Gly Thr Thr Leu Ser Ile Pro Arg Leu Ala Arg
3025 3030 3035 3040

Ala Ala Arg Pro Asp Pro Ala Ala Gly Phe Lys Thr Arg Gly Pro Val
3045 3050 3055

Leu Val Thr Gly Gly Thr Gly Ser Leu Gly Gly Leu Val Ala Arg His

3060	3065	3070
Leu Val Glu Arg His Gly Val Arg Gln Leu Val Leu Ala Ser Arg Arg		
3075	3080	3085
Gly Leu Asp Ala Glu Gly Ala Lys Asp Leu Val Thr Asp Leu Thr Ala		
3090	3095	3100
Leu Gly Ala Asp Val Ala Val Ala Ala Cys Asp Val Ala Asp Arg Asp		
3105	3110	3115 3120
Gln Val Ala Ala Leu Leu Thr Glu His Arg Pro Ser Ala Val Val His		
3125	3130	3135
Thr Ala Gly Val Pro Asp Ala Gly Val Ile Gly Thr Val Thr Pro Asp		
3140	3145	3150
Arg Leu Ala Glu Val Phe Ala Pro Lys Val Thr Ala Ala Arg His Leu		
3155	3160	3165
Asp Glu Leu Thr Arg Asp Leu Asp Leu Asp Ser Phe Val Val Tyr Ser		
3170	3175	3180
Ser Val Ser Ala Val Phe Met Gly Ala Gly Ser Gly Ser Tyr Ala Ala		
3185	3190	3195 3200
Ala Asn Ala Tyr Leu Asp Gly Leu Met Ala His Arg Arg Ala Ala Gly		
3205	3210	3215
Leu Pro Gly Gln Ser Leu Ala Trp Gly Leu Trp Asp Gln Thr Thr Gly		
3220	3225	3230
Gly Met Ala Ala Gly Thr Asp Glu Ala Gly Arg Ala Arg Met Thr Arg		
3235	3240	3245
Arg Gly Gly Leu Val Ala Met Lys Pro Ala Ala Gly Leu Asp Leu Phe		
3250	3255	3260

3060 3065 3070 3075 3080 3085 3090 3095 3100 3105 3110 3115 3120 3125 3130 3135 3140 3145 3150 3155 3160 3165 3170 3175 3180 3185 3190 3195 3200 3205 3210 3215 3220 3225 3230 3235 3240 3245 3250 3255 3260

Asp Ala Ala Ile Gly Ser Gly Glu Pro Leu Leu Val Pro Ala Gln Leu
3265 3270 3275 3280

Asp Leu Arg Gly Leu Arg Ala Glu Ala Ala Gly Gly Thr Glu Val Pro
 3285 3290 3295

His Leu Leu Arg Gly Leu Val Arg Ala Gly Arg Gln Gln Ala Arg Ala
 3300 3305 3310

Ala Ser Thr Val Glu Glu Asn Trp Ala Gly Arg Leu Ala Gly Leu Glu
 3315 3320 3325

Pro Ala Glu Arg Gly Gln Val Leu Leu Glu Leu Val Arg Ala Gln Val
 3330 3335 3340

Ala Gly Val Leu Gly Tyr Arg Ala Ala His Gln Val Asp Pro Asp Gln
3345 3350 3355 3360

Gly Leu Phe Glu Ile Gly Phe Asp Ser Leu Thr Ala Ile Glu Leu Arg
 3365 3370 3375

Asn Arg Leu Arg Ala Arg Thr Glu Arg Lys Ile Ser Pro Gly Val Val
 3380 3385 3390

Phe Asp His Pro Thr Pro Ala Leu Leu Ala Ala His Leu Asn Glu Leu
 3395 3400 3405

Leu Arg Lys Lys Val
 3410

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Met Ala Ile Pro Tyr Ser Ser Leu Ala Tyr Glu Leu Arg Asp Ala Val
1 5 10 15

Asn Val Val Asp Leu Asp Glu Asp Asp Val Phe Val Thr Ser Ile Ala
20 25 30

Glu Gly Gln Gly Gly Ala Cys Tyr His Leu Asn Arg Leu Phe His Arg
35 40 45

Leu Leu Thr Glu Leu Gly Tyr Asp Val Thr Pro Leu Ala Gly Ser Thr
50 55 60

Ala Glu Gly Arg Glu Thr Phe Gly Thr Asp Val Glu His Met Phe Asn
65 70 75 80

Leu Val Thr Leu Asp Gly Ala Asp Trp Leu Val Asp Val Gly Tyr Pro
85 90 95

Gly Pro Thr Tyr Val Glu Pro Leu Ala Val Ser Pro Ala Val Gln Thr
100 105 110

Gln Tyr Gly Ser Gln Phe Arg Leu Val Glu Gln Glu Thr Gly Tyr Ala
115 120 125

Leu Gln Arg Arg Gly Ala Val Thr Arg Trp Ser Val Val Tyr Thr Phe
130 135 140

Thr Thr Gln Pro Arg Gln Trp Ser Asp Trp Lys Glu Leu Glu Asp Asn

150

155

160

Phe Arg Ala Leu Val Gly Asp Thr Thr Arg Thr Asp Thr Gln Glu Thr

Leu Cys Gly Arg Ala Phe Ala Asn Gly Gln Val Phe Leu Arg Gln Arg

Arg Tyr Leu Thr Val Glu Asn Gly Arg Glu Gln Val Arg Thr Ile Thr

Asp Asp Asp Glu Phe Arg Ala Leu Val Ser Arg Val Leu Ser Gly Asp

His Gly

(The following are the names of the persons who have been elected to the various offices of the Association, as reported by the Secretary.)